

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:12 ; Search time 180.906 Seconds  
(without alignments)  
686.395 Million cell updates/sec

Title: US-10-611-655-10  
Perfect score: 944  
Sequence: 1 MHGEGTFTSDVSSYLEGQAA.....VKCEGISLLAQNTSHHHHH 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	630	66.7	161	1 THY1 HUMAN	P04216 homo sapien
2	624	66.1	161	2 Q5R508 PONYA	Q5R508 pongo pygma
3	619	65.6	161	1 THY1 MACMU	O62643 macaca mula
4	546	57.8	145	2 Q59GA0 HUMAN	Q59GA0 homo sapien
5	503	53.3	161	2 Q9WUR5 CAVPO	Q9WUR5 cavia porce
6	421	44.6	161	1 THY1 RAT	P01830 rattus norv
7	406.5	43.1	162	1 THY1 MOUSE	P01831 mus musculu
8	406.5	43.1	162	2 Q53XK2 MOUSE	Q53XK2 mus musculu
9	320	33.9	160	2 Q7T252 CHICK	Q7T252 gallus gall
10	305.5	32.4	160	1 THY1 CHICK	Q07212 gallus gall
11	244	25.8	60	2 Q9XT67 CANFA	Q9xt67 canis fami
12	157	16.6	45	2 Q6PPF4 CAPHI	Q6ppf4 capra hircu
13	157	16.6	176	1 GLUC SHREP	O8mj25 o glucagon
14	157	16.6	180	1 GLUC BOVIN	P01272 b glucagon
15	157	16.6	180	1 GLUC CANFA	P29794 c glucagon
16	157	16.6	180	1 GLUC CAVPO	P05110 c glucagon
17	157	16.6	180	1 GLUC HUMAN	P01275 h glucagon
18	157	16.6	180	1 GLUC MESAU	P01273 m glucagon
19	157	16.6	180	1 GLUC MOUSE	P55095 m glucagon
20	157	16.6	180	1 GLUC OCTDE	P22890 o glucagon
21	157	16.6	180	1 GLUC PIG	P01274 s glucagon
22	157	16.6	180	1 GLUC RAT	P06883 r glucagon
23	157	16.6	180	2 Q53TP6 HUMAN	Q53TP6 homo sapien
24	145.5	15.4	124	2 Q6RYB1_9SAUR	Q6ryb1 agkistrodon
25	145	15.4	206	1 GLUC CHICK	P68259 g glucagon
26	144	15.3	80	2 Q61UF8 PHOSU	G61up8 phodopus su
27	139	14.7	145	2 Q6RYB5 NEOPS	Q6ryb5 neoceratodu
28	139	14.7	204	1 GLUC HELSU	O12956 h glucagon
29	136	14.4	153	2 Q6RYB6 PRODO	Q6ryb6 protopetrus
30	135	14.3	255	2 Q6KB05 MOUSE	Q6kb05 mus musculu
31	125	13.2	103	1 GLUC_RANCA	P15438 rana catesb

32	125	13.2	220	2 Q8UWL9_9NEOB	Q8uwl9 hoplobatr
33	123	13.0	120	2 Q6RYB7 ICTPU	Q6ryb7 ictalurus p
34	122	12.9	30	1 GLUCL_ANGAN	P63294 anguilla an
35	122	12.9	30	1 GLUCL_ANGRO	P63295 anguilla ro
36	122	12.9	122	1 GLUC2_LOPAM	P04092 lophius ame
37	122	12.9	123	2 Q6RYA9_9PERC	Q6rya9 sebastes ca
38	122	12.9	860	2 Q4RQV4_TETNG	Q4rqv4 tetraodon n
39	121	12.8	149	2 Q6RYB2_BUFMA	Q6ryb2 bufo marinu
40	121	12.8	266	1 GLUCL_XENLA	O42143 xenopus lae
41	121	12.8	266	2 Q6DI24_XENTR	Q6di24 xenopus tro
42	118	12.5	487	2 Q65ZL2_9MURI	Q65zl2 mus sp. fv/
43	116	12.3	219	1 GLUC2_XENLA	O42144 xenopus lae
44	116	12.3	219	2 Q5D082_XENLA	Q5d082 xenopus lae
45	115	12.2	33	1 GLUC2_ORENI	P81027 oreochromis

## ALIGNMENTS

RESULT 1  
THY1\_HUMAN STANDARD; PRT; 161 AA.  
AC P04216; Q16008; Q9NSP1;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CDw90) (CD90 antigen).  
GN Name=THY1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86016759; PubMed=2864690;  
RA Seki T., Spurr N., Obata F., Goyert S., Goodfellow P., Silver J.;  
RT "The human Thy-1 gene: structure and chromosomal location.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:6657-6661(1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20403900; PubMed=10944468; DOI=10.1006/bbrc.2000.3282;  
RA Ye Z., Connor J.R.;  
RT "cDNA cloning by amplification of circularized first strand cDNAs reveals non-IRE-regulated iron-responsive mRNAs.";  
RL Biochem. Biophys. Res. Commun. 275:223-227(2000).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Amygdala;  
RG The German cDNA consortium;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Brain, and Eye;  
RX MEDLINE=12477932; PubMed=1247388257; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G., Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toohiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RX NUCLEOTIDE SEQUENCE OF 1-55.  
RY MEDLINE=93240114; PubMed=7683034; DOI=10.1084/jem.177.5.1331;  
RA Craig W., Kay R., Cutler R.L., Langedorp P.M.;  
RT "Expression of Thy-1 on human hematopoietic progenitor cells.";  
RL J. Exp. Med. 177:1331-1342(1993).  
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions  
CC during synaptogenesis and other events in the brain.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)  
CC domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; M11749; AA61180.1; -; Genomic DNA.  
DR EMBL; AF261093; AAG13904.1; -; mRNA.  
DR EMBL; AL161958; CAB82306.1; -; mRNA.  
DR EMBL; BC005175; AAH05175.1; -; mRNA.  
DR EMBL; BC065559; AAH65559.1; -; mRNA.  
DR EMBL; S59749; AAB26333.2; -; mRNA.  
DR F1R; A02106; TDHU.  
DR P1R; T47130; T47130.  
DR Ensembl; ENSG00000154096; Homo sapiens.  
DR HGNC; HGNC:11801; THY1.  
DR H-InvDB; HIX0010195; -.  
DR MIM; 188230; -.  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0005886; C:plasma membrane; NAS.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF000047; Ig; 1.  
DR SMART; SM00409; Ig; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein;  
KW Membrane; Signal; T-cell.  
FT SIGNAL 1 19  
FT CHAIN 20 130 Thy-1 membrane glycoprotein.  
FT PROPEP 131 161 Removed in mature form.  
FT DOMAIN 130 126 Ig-like V-type.  
FT LIPID 130 130 GPI-anchor amidated cysteine.  
FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 119 119 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).  
FT DISULFID 28 104 By similarity.  
FT DISULFID 38 104 By similarity.  
FT CONFLICT 54 55 LT -> AP (in Ref. 5).  
FT CONFLICT 85 85 N -> H (in Ref. 1).  
SQ SEQUENCE 161 AA; 17935 MW; 2B6796DA8E7454B CRC64;  
  
Query Match 66.7%; Score 630; DB 1; Length 161;  
Best Local Similarity 99.2%; Pred. No. 2.4e-47;  
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 49 QKVTSLTACLVDSQLDCRHEHTSSPIQYEFSLTRTKKHVLFGTGVGPHTYRSRTN 108  
DB 20 QKVTSLTACLVDSQLDCRHEHTSSPIQYEFSLTRTKKHVLFGTGVGPHTYRSRTN 79  
  
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDLKVKCEGISLLAQN 168  
DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDLKVKCEGISLLAQN 139  
  
QY 169 TS 170  
DB 140 TS 141  
  
RESULT 3  
THY1\_MACMU  
ID THY1\_MACMU STANDARD; PRT; 161 AA.  
AC 062643;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90) (CD90 antigen).  
GN Name=THY1;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Thymus;  
RA Margulies B.J., Clements J.E.;  
RT "Rhesus macaque CD90.";  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBSJ databases.  
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions  
CC during synaptogenesis and other events in the brain.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)

RESULT 2  
QSR508\_PONPY  
ID QSR508\_PONPY PRELIMINARY; PRT; 161 AA.  
AC QSR508;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Hypothetical protein DKFZp459C1015.  
GN Name=DKFZp459C1015;  
OS Pongo pygmaeus (Orangutan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
OC Pongo  
OX NCBI\_TaxID=9600;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Cortex;  
RG The German cDNA Consortium;  
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,  
RA Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (NOV-2004) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; CR861077; CAH93158.1; -; mRNA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF000047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Hypothetical protein; Immunoglobulin domain.  
SQ SEQUENCE 161 AA; 17963 MW; 2B6791DD8CB0401B CRC64;  
  
Query Match 66.1%; Score 624; DB 2; Length 161;  
Best Local Similarity 97.5%; Pred. No. 8e-47;  
Matches 119; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 49 QKVTSLTACLVDSQLDCRHEHTSSPIQYEFSLTRTKKHVLFGTGVGPHTYRSRTN 108  
DB 20 QKVTSLTACLVDSQLDCRHEHTSSPIQYEFSLTRTKKHVLFGTGVGPHTYRSRTN 79  
  
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDLKVKCEGISLLAQN 168  
DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDLKVKCEGISLLAQN 139  
  
QY 169 TS 170  
DB 140 TS 141  
  
RESULT 3  
THY1\_MACMU  
ID THY1\_MACMU STANDARD; PRT; 161 AA.  
AC 062643;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90) (CD90 antigen).  
GN Name=THY1;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopithecoidea; Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Thymus;  
RA Margulies B.J., Clements J.E.;  
RT "Rhesus macaque CD90.";  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBSJ databases.  
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions  
CC during synaptogenesis and other events in the brain.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)

CC domain.  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.

CC -----  
CC EMBL; U93310; AAC05640.1; -; mRNA.  
CC InterPro; IPR003599; IG.  
CC InterPro; IPR007110; IG-like.  
CC Pfam; PF00047; ig; 1.  
CC SMART; SM00409; IG; 1.  
CC PROSITE; PS00835; IG LIKE; 1.  
CC Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein;  
CC Membrane; Signal; T-cell.  
CC SIGNAL 1 19  
CC CHAIN 20 130 Thy-1 membrane glycoprotein.  
CC PROPEP 131 161 Removed in mature form.  
CC DOMAIN 20 126 Ig-like V-type.  
CC LIPID 130 130 GPI-anchor amidated cysteine.  
CC CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
CC CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).  
CC CARBOHYD 119 119 N-linked (GlcNAc...) (Potential).  
CC CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).  
CC DISULFID 28 130 By similarity.  
CC DISULFID 38 104 By similarity.  
CC SEQUENCE 161 AA; 18011 MW; 326B135498BA401B CRC64;

Query Match 65.6%; Score 619; DB 1; Length 161;  
Best Local Similarity 96.7%; Pred. No. 2.2e-46;  
Matches 118; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHYRSRTN 108  
DB 20 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHYRSRTN 79  
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168  
DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139

QY 169 TS 170  
DB 140 TS 141

RESULT 4  
Q59GA0 HUMAN PRELIMINARY; PRT; 145 AA.  
AC Q59GA0;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Thy-1 cell surface antigen variant (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,  
RA Ohara O., Negase T., Kikuno F.R.;  
RT "None Title."  
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
FR EMBL; AB209209; BAD92446.1; -; mRNA.  
FT NON TER 1 1  
FT SEQUENCE 145 AA; 15904 MW; 9DA4BC208DCD5766 CRC64;

Query Match 57.8%; Score 546; DB 2; Length 145;  
Best Local Similarity 99.0%; Pred. No. 4.9e-40;  
Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHYRSRTN 108  
DB 36 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHYRSRTN 95  
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLR 153  
DB 96 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLR 140

## RESULT 5

Q9WUR5 CAVPO  
ID Q9WUR5\_CAVPO PRELIMINARY; PRT; 161 AA.  
AC Q9WUR5;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Thy-1 protein precursor.  
DE Name=Thy-1;  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
OC Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Spleen;  
RA Schaefer H., Burger R., Otto A., Bartels T.;  
RT "Characterization and cloning of guinea pig Thy-1."  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ238589; CAB44008.1; -; mRNA.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00409; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Immunoglobulin domain; Signal.  
FT SIGNAL 1 19 Potential.  
FT CHAIN 20 161 Thy-1 protein.  
SQ SEQUENCE 161 AA; 17995 MW; 241461D901P80B1B CRC64;

Query Match 53.3%; Score 503; DB 2; Length 161;  
Best Local Similarity 79.5%; Pred. No. 3.3e-36;  
Matches 97; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHYRSRTN 108  
DB 20 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETKKHLFGTVGVPEHYRSRTN 79  
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168  
DB 80 LTSNYNIKVLYLANFTTKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139

QY 169 TS 170  
DB 140 TS 141

## RESULT 6

THY1\_RAT  
ID THY1\_RAT STANDARD; PRT; 161 AA.  
AC P01830;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90 antigen).  
DE Name=Thy1;  
GN Name=Thy1; Synonyms=Thy-1;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;

RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=86005549; PubMed=2864289;  
 RX Seki T., Chang H.-C., Moriuchi T., Denome R., Silver J.;  
 RA "Thy-1: a hydrophobic transmembrane segment at the carboxyl  
 terminus";  
 RT Fed. Proc. 44:2865-2869(1985).  
 RL Nature 301:80-82(1983).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE OF 1-122.  
 RX MEDLINE=83115223; PubMed=6130472;  
 RA Moriuchi T., Chang H.-C., Denome R., Silver J.;  
 RT "Thy-1 cDNA sequence suggests a novel regulatory mechanism.";  
 RL Nature 301:80-82(1983).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE OF 20-161.  
 RX MEDLINE=85111162; PubMed=2857477;  
 RA Seki T., Moriuchi T., Chang H.-C., Denome R., Silver J.;  
 RT "Structural organization of the rat thy-1 gene";  
 RL Nature 313:485-487(1985).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE OF 20-161.  
 RX MEDLINE=85051865; PubMed=6149956; DOI=10.1016/0014-5793(84)81250-8;  
 RA Moriuchi T., Silver J.;  
 RT "Rat Thy-1 antigen has a hydrophobic segment at the carboxyl  
 terminus";  
 RL FEBS Lett. 178:105-108(1984).  
 RN [5]  
 RP PROTEIN SEQUENCE OF 20-130.  
 RX MEDLINE=82068190; PubMed=6118137;  
 RA Campbell D.G., Gagnon J., Reid K.B.M., Williams A.F.;  
 RT "Rat brain Thy-1 glycoprotein. The amino acid sequence, disulphide  
 bonds and an unusual hydrophobic region.";  
 RL Biochem. J. 195:15-30(1981).  
 RN [6]  
 RP STRUCTURE OF CARBOHYDRATES.  
 RX MEDLINE=87275814; PubMed=2886334;  
 RA Parekh R.B., Tee A.G.D., Dwek R.A., Williams A.F., Rademacher T.W.;  
 RT "Tissue-specific N-glycosylation, site-specific oligosaccharide  
 patterns and lentil lectin recognition of rat Thy-1.";  
 RL EMBO J. 6:1233-1244(1987).  
 CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions  
 during synaptogenesis and other events in the brain.  
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -!- TISSUE SPECIFICITY: Abundant in lymphoid tissues.  
 CC -!- PTM: Glycosylation is tissue specific. Sialylation of N-glycans at  
 Asn-93 in brain and at Asn-42, Asn-93 and Asn-117 in thymus.  
 CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)  
 domain.  
 CC -----  
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC -----  
 DR EMBL; X03152; CAA26931.1; -; Genomic\_DNA.  
 DR EMBL; X03150; CAA26929.1; -; mRNA.  
 DR EMBL; X02002; CAA26033.1; -; Genomic\_DNA.  
 DR EMBL; M18002; AAA42243.1; -; mRNA.  
 DR EMBL; M10666; AAA42242.1; -; mRNA.  
 DR FIR; B45909; TDET.  
 DR Ensembl; ENSRNOG0000006504; Rattus norvegicus.  
 DR RGD; 3860; Thy1.  
 DR GO; GO:0009986; C:cell surface; TAS.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR SMART; SM00409; IG\_1.  
 DR PROSITE; P550835; IG\_LIKE; 1.  
 DR Direct protein sequencing; Glycoprotein; GPI-anchor;  
 KW Immunoglobulin domain; Lipoprotein; Membrane;  
 KW Pyrrolidone carboxylic acid; Sialic acid; Signal; T-cell.  
 FT SIGNAL 1 19  
 FT CHAIN 20 130 Thy-1 membrane glycoprotein.

FT PROPEP 131 161 Removed in mature form.  
 FT DOMAIN 20 126 Ig-like V-type.  
 FT MOD\_RES 20 20 Pyrrolidone carboxylic acid.  
 FT LIPID 130 130 GPI-anchor amidated cysteine.  
 FT CARBOHYD 42 42 N-linked (GlcNAc...) (high mannose or  
 complex); in thymus.  
 FT CARBOHYD 42 42 N-linked (GlcNAc...) (high mannose); in  
 brain.  
 FT CARBOHYD 93 93 N-linked (GlcNAc...) (complex).  
 FT CARBOHYD 117 117 N-linked (GlcNAc...) (complex); in  
 thymus.  
 FT CARBOHYD 117 117 N-linked (GlcNAc...) (high mannose or  
 hybrid); in brain.  
 FT DISULFID 28 130  
 FT DISULFID 38 104  
 FT CONFLICT 71 71  
 SQ SEQUENCE 161 AA; 18172 MW; 3285748F3C2C5AB2 CRC64; E -> Q (in Ref. 1).  
 Query Match 44.6%; Score 421; DB 1; Length 161;  
 Best Local Similarity 67.2%; Pred. No. 5.1e-25; Indels 0; Gaps 0;  
 Matches 82; Conservative 15; Mismatches 25;  
 QY 49 QKVTSLTACLVDQSLRLDCRHHNTSSSPIQYEFSLTRETKKHLVFTGVGPETHYRSRTN 108  
 DB 20 QRVISLTACLAVNQNLRLDCRHHNTNLPQHEFSLTREKKKHLVSGTLGVPETHYRSRVN 79  
 QY 109 FTSKHYMKVLYLSAFTSKDEGTTCALHSHGSHSPPISSQNVTVLRDLKVKCGISLLAQN 168  
 DB 80 LFSDFIRKVLTAFTTDEGDYMCSELVSGQNPSTSSNKTINVRDLKVKCGISLLVQN 139  
 QY 169 TS 170  
 DB 140 TS 141  
 RESULT 7  
 THYL MOUSE  
 ID THYL\_MOUSE STANDARD; PRT; 162 AA.  
 AC P01831;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90  
 antigen).  
 DE Name=Thy1; Synonyms=Thy-1;  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=85115360; PubMed=2857501;  
 RA Seki T., Chang H.-C., Moriuchi T., Denome R., Ploegh H., Silver J.;  
 RT "A hydrophobic transmembrane segment at the carboxyl terminus of thy-  
 1.";  
 RL Science 227:649-651(1985).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPE).  
 RX STRAIN=BALB/c;  
 RX MEDLINE=86055760; PubMed=2866091;  
 RA Giguere V., Isobe K.-I., Grosveld F.;  
 RT "Structure of the murine Thy-1 gene";  
 RL EMBO J. 4:2017-2024(1985).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPE).  
 RX MEDLINE=85216583; PubMed=2582427;  
 RA Chang H.-C., Seki T., Moriuchi T., Silver J.;  
 RT "Isolation and characterization of mouse Thy-1 genomic clones.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3819-3823(1985).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPE).  
 RX MEDLINE=86113437; PubMed=2868059;



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ID Q7T252_CHICK PRELIMINARY; PRT; 160 AA.
AC Q7T252;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE THY1.
GN Name=Thy1;
OS Gallus gallus (Chicken).
OC Archosauromorpha; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_Thy1;
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14711516; DOI=10.1016/j.pep.2003.10.011;
RA Mehndiratta P., Walton W.J., Hare J.T., Fulido S., Parthasarathy G.,
RA Emmett M.R., Marshall A.G., Logan T.M.;
RT "Expression, purification, and characterization of avian Thy-1 from
RT Lec1 mammalian and Tn5 insect cells.";
RL Protein Expr. Purif. 33:274-287(2004).
DR EMBL; AY230132; AAP31241.1; -; mRNA.
DR Ensembl; ENSGALG00000006751; Gallus gallus.
DR InterPro; IPR003599; IG.
DR SMART; SM00409; IG.
DR Pfam; PF00047; IG.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Immunoglobulin domain.
SQ SEQUENCE 160 AA; 18061 MW; 6DC39D8519540CE6 CRC64;

Query Match 33.9%; Score 320; DB 2; Length 160;
Best Local Similarity 48.4%; Pred. No. 3.7e-20;
Matches 59; Conservative 24; Mismatches 39; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDSQSLRDLCDRHEHNTSSPIQYFSLTRTKKHVLFQTVGVPHYRSRTN 108
Db 20 QMIRDLASCLLQSLRVDRCYENKTSNPLTYEFSLTRQ-QKHIIQSTISVSENVYRNAN 79

QY 109 FTSKYHMKVLYLSAFTSKDEGYTCALHSHGSHSPPISSQNVTVLRDLKVKCGISLLAQN 168
Db 80 VTMHKNLVCLYLHSLFTSDGVMCELMKATNDYTGNIKNITVTKLEKCKAGFSLLIQN 139

QY 169 TS 170
Db 140 TS 141

RESULT 10
THY1_CHICK
ID THY1_CHICK STANDARD; PRT; 160 AA.
AC Q07212;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen).
GN Name=Thy1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_Thy1;
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 43-55; 59-79 AND 81-101.
RC STRAIN=White Leghorn; TISSUE=Brain;
RX MEDLINE=93061794; PubMed=1359371; DOI=10.1016/0169-328X(92)90180-J;
RA Dowling B.J., Gooley A.A., Gunning P., Cunningham A., Jeffrey P.L.;
RT "Molecular cloning and primary structure of the avian Thy-1
RT glycoprotein.";
RL Brain Res. Mol. Brain Res. 14:250-260(1992).
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions
CC during synaptogenesis and other events in the brain.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
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CC -!- TISSUE SPECIFICITY: Forebrain, cerebellum and tectum.
CC -!- DEVELOPMENTAL STAGE: It is detected at embryonic day 4 (E4) in
CC forebrain and tectum. There is an increase in levels between E16
CC and the first few days post-hatch. During E19 to hatch a rapid
CC reduction in the levels is seen with a general increase in
CC expression in adulthood.
CC -!- PTM: The N-terminus is blocked.
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)
CC domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; S47368; AA111889.1; -; mRNA.
CC EMBL; L14924; AAC42216.1; -; mRNA.
CC PIR; A48975; A48975.
CC Ensembl; ENSGALG00000006751; Gallus gallus.
CC InterPro; IPR003599; IG.
CC SMART; SM00409; IG.
CC Direct protein sequencing; Glycoprotein; GPI-anchor;
CC Immunoglobulin domain; Lipoprotein; Membrane;
CC Pyroglutamate carboxylic acid; Signal; T-cell.
KW Pyroglutamate carboxylic acid; Signal; T-cell.
FT SIGNAL 1 19
FT CHAIN 20 129
FT PROPEP 130 160
FT MOD_RES 20 20
FT LIPID 129 129
FT GPI-anchor amidated cysteine (By
FT similarity)
FT CARBOHYD 42 42
FT CARBOHYD 78 78
FT CARBOHYD 118 118
FT CARBOHYD 138 138
FT DISULFID 28 129
FT DISULFID 38 103
FT CONFLICT 76 76
FT CONFLICT 82 82
FT SEQUENCE 160 AA; 18165 MW; E378D241CC2D4739 CRC64;

Query Match 32.4%; Score 305.5; DB 1; Length 160;
Best Local Similarity 48.4%; Pred. No. 6.9e-19;
Matches 59; Conservative 25; Mismatches 37; Indels 1; Gaps 1;

QY 49 QKVTSLTACLVDSQSLRDLCDRHEHNTSSPIQYFSLTRTKKHVLFQTVGVPHYRSRTN 108
Db 20 QMIRDLASCLLQSLRVDRCYENKTSNPLTYEFSLTRQ-QKHIIQSTISVSENVYRNAN 78

QY 109 FTSKYHMKVLYLSAFTSKDEGYTCALHSHGSHSPPISSQNVTVLRDLKVKCGISLLAQN 168
Db 79 VTMHKNLVCLYLHSLFTSDGVMCELMKATNDYTGNIKNITVTKLEKCKAGFSLLIQN 138

QY 169 TS 170
Db 139 TS 140

RESULT 11
Q9XT67_CANFA
ID Q9XT67_CANFA PRELIMINARY; PRT; 60 AA.
AC Q9XT67;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thy-1 (Fragment).
GN Name=Thy1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
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RN RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99265967; PubMed=10331940; DOI=10.1006/geno.1999.5772;
RA Li R., Mignot E., Pakaco J., Kadotani H., Cantanese J., Zhao B.,
RA Lin X., Hinton L., Ostrander E.A., Patterson D.F., de Jong P.J.,
RT "Construction and characterization of an eightfold redundant dog
RT genomic bacterial artificial chromosome library.;"
RL Genomics 58:9-17(1999).
RN [2]
RN RP NUCLEOTIDE SEQUENCE.
RA Kodatani H., Mignot E.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103747; AD40573.1; -; Genomic DNA.
DR Ensembl; ENSCAPG000012021; Canis familiaris.
FT NON_TER 1
FT NON_TER 60
SQ SEQUENCE 60 AA; 6700 MW; 97AFAD948FD8D054 CRC64;
Query Match 25.8%; Score 244; DB 2; Length 60;
Best Local Similarity 78.3%; Pred. No. 5.3e-14;
Matches 47; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 94 GTGVPETHYRSTNFTSKYHMKVLYLSAFTSKDECTYTCALHHSCHSPISQNVTVLR 153
DB 1 GTGVPETHYRSTNFTSKYHMKVLYLSAFTSKDECTYTCALHHSCHSPISQNVTVLR 60
RESULT 12
ID Q6PPF4_CAPHI PRELIMINARY; PRT; 45 AA.
AC Q6PPF4;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Glucagon (Fragment).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RN RP NUCLEOTIDE SEQUENCE.
RA Ballester M., Castello A., Ibanez E., Sanchez A., Folch J.M.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY588290; AAT00451.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; Hormone 2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5179 MW; B538A926E9447F80 CRC64;
Query Match 16.6%; Score 157; DB 2; Length 45;
Best Local Similarity 96.8%; Pred. No. 1.6e-06;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 HGRGTFTSDVSSYLEGQAAKEFTAWLVKGRG 32
DB 13 HGRGTFTSDVSSYLEGQAAKEFTAWLVKGRG 43
RESULT 13
ID _GLUC SHEEP STANDARD; PRT; 176 AA.
AC QBMJ75;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Glucagon precursor [Contains: Glucicentin; Glucicentin-related polypeptide
DE (GRPP); Oxyntomodulin (OXY) (OXM); Glucagon; Glucagon-like peptide 1
DE (GLP-1); Glucagon-like peptide 1(7-37) (GLP-1(7-37)); Glucagon-like
peptide 1(7-36) (GLP-1(7-36)); Glucagon-like peptide 2 (GLP-2)]
Name=GGC;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RN RP NUCLEOTIDE SEQUENCE.
RA Limesand S.W., Hay W.W. Jr.;
RL "Characterization of the endocrine pancreas in an ovine placental
RL insufficiency IUGR fetus.;"
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Glucagon plays a key role in glucose metabolism and
CC homeostasis. Regulates blood glucose by increasing gluconeogenesis
CC and decreasing glycolysis. A counterregulatory hormone of insulin,
CC raises plasma glucose levels in response to insulin-induced
CC hypoglycemia (By similarity).
CC -!- FUNCTION: GLP-1 is a potent stimulator of glucose-dependent
CC insulin release. Play important roles on gastric motility and the
CC suppression of plasma glucagon levels. May be involved in the
CC suppression of satiety and stimulation of glucose disposal in
CC peripheral tissues, independent of the actions of insulin. Have
CC growth-promoting activities on intestinal epithelium. May also
CC regulate the hypothalamic pituitary axis (HPA) via effects on LH,
CC TSH, CRH, oxytocin, and vasopressin (By similarity).
CC -!- FUNCTION: GLP-2 stimulates intestinal growth and up-regulates
CC villus height in the small intestine, concomitant with increased
CC gastro-intestinal tract, from the stomach to the colon is the
CC principal target for GLP-2 action. Plays a key role in nutrient
CC homeostasis, enhancing nutrient assimilation through enhanced
CC gastrointestinal function, as well as increasing nutrient
CC disposal. Stimulates intestinal glucose transport and decreases
CC mucosal permeability (By similarity).
CC -!- FUNCTION: Oxyntomodulin significantly reduces food intake (By
CC similarity).
CC -!- FUNCTION: Glucicentin may modulate gastric acid secretion and
CC gastro-pyloro-duodenal activity.
CC -!- TISSUE SPECIFICITY: Glucagon is secreted in the A cells of the
CC islets of Langerhans. GLP-1, GLP-2, oxyntomodulin and glucicentin
CC are secreted from enteroendocrine cells throughout the
CC gastrointestinal tract. GLP1 and GLP2 are also secreted in
CC selected neurons in the brain.
CC -!- INDUCTION: Glucagon release is stimulated by hypoglycemia and
CC inhibited by hyperglycemia, insulin, and somatostatin. GLP-1 and
CC GLP-2 are induced in response to nutrient ingestion (By
CC similarity).
CC -!- PTM: Proglucagon is posttranslationally processed in a tissue-
CC specific manner in pancreatic A cells and intestinal L cells. In
CC pancreatic A cells, the major bioactive hormone is glucagon
CC cleaved by PCSK2/PC2. In the intestinal L cells PCSK1/PC1
CC liberates GLP-1, GLP-2, glucicentin and oxyntomodulin. GLP-1 is
CC further N-terminally truncated by posttranslational processing in
CC the intestinal L cells resulting in GLP-1(7-37) GLP-1(7-36)amide.
CC The C-terminal amidation is neither important for the metabolism
CC of GLP-1 nor for its effects on the endocrine pancreas (By
CC similarity).
CC -!- MISCELLANEOUS: GLP-2 does not have cleavage on a pair of basic
CC residues at C-terminus as in other mammals.
CC -!- SIMILARITY: Belongs to the glucagon family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF529185; AAM944409.1; -; mRNA.

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DR InterPro; IPR000532; Glucagon.  
DR Pfam; PF00123; Hormone 2; 3.  
DR PRINTS; PR00275; GLUCAGON.  
DR SMART; SM00070; GLUCA; 3.  
DR PROSITE; PS00260; GLUCAGON; 4.  
KW Amidation; Cleavage on pair of basic residues; Glucagon family;  
KW Hormone; Signal.  
FT SIGNAL 1 20  
FT PEPTIDE 21 89  
FT PEPTIDE 21 50  
FT PEPTIDE 53 89  
FT PEPTIDE 53 81  
FT PROPEP 84 89  
FT PEPTIDE 92 128  
FT PEPTIDE 98 128  
FT PEPTIDE 98 127  
FT PROPEP 131 145  
FT PEPTIDE 146 >176  
FT SITE 52 53  
FT SITE 83 84  
FT SITE 91 92  
FT SITE 97 98  
FT SITE 130 131  
FT SITE 145 146  
FT MOD\_RES 127 127  
FT NON\_TER 176 176  
FT SEQUENCE 176 AA; 20336 MW; 13174039B6CE2B3 CRC64;  
SQ  
Query Match 16.6%; Score 157; DB 1; Length 176;  
Best Local Similarity 96.8%; Pred. No. 8.2e-06;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 HGEFTSDVSSYLEGQAAKEFTAMLVKGRG 32  
DB 98 HAEGTFTSDVSSYLEGQAAKEFTAMLVKGRG 128  
RESULT 14  
ID GLUC\_BOVIN STANDARD; PRT; 180 AA.  
AC P01272;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Glucagon precursor [Contains: Glucicentin; Glucicentin-related polypeptide  
DE (GRPP); Oxyntomodulin (OXY) (OXN); Glucagon; Glucagon-like peptide 1  
DE (GLP-1); Glucagon-like peptide 1(7-37) (GLP-1(7-37)); Glucagon-like  
DE peptide 1(7-36) (GLP-1(7-36)); Glucagon-like peptide 2 (GLP-2)].  
GN Names=GGC;  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=83299996; PubMed=6577439;  
RA Lopez L.C., Frazier M.L., Su C.-J., Kumar A., Saunders G.F.;  
RT "Mammalian pancreatic preproglucagon contains three glucagon-related  
RT peptides.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:5485-5489(1983).  
RN [2]  
RP PROTEIN SEQUENCE OF 53-81.  
RX MEDLINE=71166445; PubMed=5102927;  
RA Bromer W.W., Boucher M.E., Koffenberger J.E. Jr.;  
RT "Amino acid sequence of bovine glucagon.";  
RL J. Biol. Chem. 246:2822-2827(1971).  
RN [3]  
RP REVIEW.  
RX MEDLINE=22442611; PubMed=12554744; DOI=10.1210/me.2002-0306;  
RA Drucker D.J.;  
RT "Glucagon-like peptides: regulators of cell proliferation,  
RT differentiation, and apoptosis.";  
RL Mol. Endocrinol. 17:161-171(2003).  
RN [4]  
RP REVIEW.  
RX MEDLINE=22513095; PubMed=12626323; DOI=10.1152/ajpendo.00492.2002;  
RA Jiang G., Zhang B.B.;  
RT "Glucagon and regulation of glucose metabolism.";  
RL Am. J. Physiol. 284:E671-E678(2003).  
RN [5]  
RP REVIEW.  
RX PubMed=10322410;  
RA Drucker D.J.;  
RT "Glucagon-like peptide 2.";  
RL Trends Endocrinol. Metab. 10:153-156(1999).  
RN [6]  
RP REVIEW.  
RX MEDLINE=20073561; PubMed=10605628; DOI=10.1210/er.20.6.876;  
RA Kieffer T.J., Habener J.F.;  
RT "The glucagon-like peptides.";  
RL Endocr. Rev. 20:876-913(1999).  
RN [7]  
RP STRUCTURE BY NMR OF 53-81.  
RX MEDLINE=71166445; PubMed=6631957;  
RA Braun W., Wider G., Lee K.H., Wuethrich K.;  
RT "Conformation of glucagon in a lipid-water interphase by 1H nuclear  
RT magnetic resonance.";  
RL J. Mol. Biol. 169:921-948(1983).  
CC -!- FUNCTION: Glucagon plays a key role in glucose metabolism and  
CC homeostasis. Regulates blood glucose by increasing gluconeogenesis  
CC and decreasing glycolysis. A counterregulatory hormone of insulin,  
CC raises plasma glucose levels in response to insulin-induced  
CC hypoglycemia (By similarity).  
CC -!- FUNCTION: GLP-1 is a potent stimulator of glucose-dependent  
CC insulin release. Play important roles on gastric motility and the  
CC suppression of plasma glucagon levels. May be involved in the  
CC suppression of satiety and stimulation of glucose disposal in  
CC peripheral tissues, independent of the actions of insulin. Have  
CC growth-promoting activities on intestinal epithelium. May also  
CC regulate the hypothalamic pituitary axis (HPA) via effects on LH,  
CC TSH, CRH, oxytocin, and vasopressin secretion. Increases islet  
CC mass through stimulation of islet neogenesis and pancreatic beta  
CC cell proliferation (By similarity).  
CC -!- FUNCTION: GLP-2 stimulates intestinal growth and up-regulates  
CC villus height in the small intestine, concomitant with increased  
CC crypt cell proliferation and decreased enterocyte apoptosis. The  
CC gastrointestinal tract, from the stomach to the colon is the  
CC principal target for GLP-2 action. Plays a key role in nutrient  
CC homeostasis, enhancing nutrient assimilation through enhanced  
CC gastrointestinal function, as well as increasing nutrient  
CC disposal. Stimulates intestinal glucose transport and decreases  
CC mucosal permeability (By similarity).  
CC -!- FUNCTION: Oxyntomodulin significantly reduces food intake (By  
CC similarity).  
CC -!- FUNCTION: Glucicentin may modulate gastric acid secretion and  
CC gastro-pyloro-duodenal activity.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Glucagon is secreted in the A cells of the  
CC islets of Langerhans. GLP-1, GLP-2, oxyntomodulin and glucicentin  
CC are secreted from enteroendocrine cells throughout the  
CC gastrointestinal tract.  
CC -!- INDUCTION: Glucagon release is stimulated by hypoglycemia and  
CC inhibited by hyperglycemia, insulin, and somatostatin. GLP-1 and  
CC GLP-2 are induced in response to nutrient ingestion (By  
CC similarity).  
CC -!- PTM: Proglucagon is posttranslationally processed in a tissue-  
CC specific manner in pancreatic A cells and intestinal L cells. In  
CC pancreatic A cells, the major bioactive hormone is glucagon  
CC cleaved by PCSK2/PC2. In the intestinal L cells PCSK1/PC1  
CC liberates GLP-1, GLP-2, glucicentin and oxyntomodulin. GLP-1 is

further N-terminally truncated by posttranslational processing in the intestinal L cells resulting in GLP-1(7-37) GLP-1(7-36)amide. The C-terminal amidation is neither important for the metabolism of GLP-1 nor for its effects on the endocrine pancreas (By similarity). Belongs to the glucagon family.

-1- SIMILARITY: Belongs to the glucagon family.

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EMBL; K00107; AAA30538.1; -; mRNA.

PDB; 1KX6; NMR; A=53-81.

InterPro; IPR000532; Glucagon.

Pfam; PF00123; Hormone 2; 3.

PRINTS; PR00275; GLUCAGON.

PROSITE; PS00260; GLUCAGON; 4.

3D-structure; Amidation; Cleavage on pair of basic residues;

Direct protein sequencing; Glucagon family; Hormone; Signal.

SIGNAL 1 20

PEPTIDE 21 89 Glucagon-like peptide 1 (By similarity)

PEPTIDE 21 50 Glucagon-like peptide 2 (By similarity)

PEPTIDE 53 89 Oxyntomodulin (By similarity)

PEPTIDE 53 81 Glucagon

PROPR 84 89 By similarity

PEPTIDE 92 128 Glucagon-like peptide 1 (By similarity)

PEPTIDE 98 128 Glucagon-like peptide 1 (7-37) (By similarity)

PEPTIDE 98 127 Glucagon-like peptide 1 (7-36) (By similarity)

PEPTIDE 131 145 By similarity

PEPTIDE 146 178 Glucagon-like peptide 2 (By similarity)

SITE 52 53 Cleavage (by PCSK2) (By similarity)

SITE 83 84 Cleavage (by PCSK1 and PCSK2) (By similarity)

SITE 91 92 Cleavage (by PCSK1) (By similarity)

SITE 97 98 Cleavage (by PCSK1) (By similarity)

SITE 130 131 Cleavage (by PCSK1) (By similarity)

SITE 145 146 Cleavage (by PCSK1) (By similarity)

MOD\_RES 127 127 Arginine amide (G-128 provides amide group) (By similarity)

TURN 60 64

TURN 74 74

HELEX 75 78

SEQUENCE 180 AA; 20944 MW; 8D9B4FF05B9F15FF CRC64;

Query Match 16.6%; Score 157; DB 1; Length 180;

Best Local Similarity 96.8%; Pred. No. 8.4e-06;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HSGGTFTSDVSSYLEGQAQKEFIATLVKGRG 32

Db 98 HASEGTFTSDVSSYLEGQAQKEFIATLVKGRG 128

RESULT 15

GLUC CANFA

ID -GLUC CANFA STANDARD; PRT; 180 AA.

AC P29794; Q95LQ0;

DT 01-APR-1993 (Rel. 25, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Glucagon precursor [Contains: Glucagon; Glucagon-like peptide 1 (GLP-1); Oxyntomodulin (OXT) (OXM); Glucagon; Glucagon-like peptide 1 (7-37) (GLP-1(7-37)); Glucagon-like peptide 1(7-36) (GLP-1(7-36)); Glucagon-like peptide 2 (GLP-2)]

DE (GLP-1); Glucagon-like peptide 1 (7-37) (GLP-1(7-37)); Glucagon-like peptide 1(7-36) (GLP-1(7-36)); Glucagon-like peptide 2 (GLP-2)]

DE Name=CCG;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Canidae;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Canidae;

Canis.  
NCBI\_TaxID=9615;  
[1] NUCLEOTIDE SEQUENCE.  
TISSUE=Pancreas, and Stomach;  
PubMed=11916259;  
Irwin D.M.;  
"CDNA cloning of proglucagon from the stomach and pancreas of the dog.";  
DNA Seq. 12:253-260(2001).  
[2] PROTEIN SEQUENCE OF 21-89.  
TISSUE=ileum;  
MEDLINE=89185675; PubMed=3238052; DOI=10.1016/0167-0115(88)90230-3;  
Shinomura Y., Eng J., Yalow R.S.;  
"Immunoreactive glucagons purified from dog pancreas, stomach and ileum.";  
Regul. Pept. 23:299-308(1988).  
[3] PROCESSING BY PCSK1 AND PCSK2.  
PubMed=10499540; DOI=10.1210/en.140.10.4800;  
Damholt A.B., Buchan A.M., Holst J.J., Kofod H.;  
"Proglucagon processing profile in canine L cells expressing endogenous prohormone convertase 1/3 and prohormone convertase 2.";  
Endocrinology 140:4800-4808(1999).  
[4] REVIEW.  
PubMed=12554744; DOI=10.1210/me.2002-0306;  
Drucker D.J.;  
"Glucagon-like peptides: regulators of cell proliferation, differentiation, and apoptosis.";  
Mol. Endocrinol. 17:161-171(2003).  
[5] REVIEW.  
PubMed=12626323; DOI=10.1152/ajpendo.00492.2002;  
Jiang G., Zhang B.B.;  
"Glucagon and regulation of glucose metabolism.";  
Am. J. Physiol. 284:E671-E678(2003).  
[6] REVIEW.  
PubMed=10322410;  
Drucker D.J.;  
"Glucagon-like peptide 2.";  
Trends Endocrinol. Metab. 10:153-156(1999).  
[7] REVIEW.  
PubMed=10605628; DOI=10.1210/er.20.6.876;  
Kieffer T.J., Habener J.F.;  
"The glucagon-like peptides.";  
Endocr. Rev. 20:876-913(1999).  
-1- FUNCTION: Glucagon plays a key role in glucose metabolism and homeostasis. Regulates blood glucose by increasing gluconeogenesis and decreasing glycolysis. A counterregulatory hormone of insulin, raises plasma glucose levels in response to insulin-induced hypoglycemia (By similarity).  
-1- FUNCTION: GLP-1 is a potent stimulator of glucose-dependent insulin release. Play important roles on gastric motility and the suppression of plasma glucagon levels. May be involved in the peripheral tissues, independent of the actions of insulin. Have growth-promoting activities on intestinal epithelium. May also regulate the hypothalamic pituitary axis (HPA) via effects on LH, TSH, CRH, oxytocin, and vasopressin secretion. Increases islet mass through stimulation of islet neogenesis and pancreatic beta cell proliferation (By similarity).  
-1- FUNCTION: GLP-2 stimulates intestinal growth and up-regulates villus height in the small intestine, concomitant with increased crypt cell proliferation and decreased enterocyte apoptosis. The gastrointestinal tract, from the stomach to the colon is the principal target for GLP-2 action. Plays a key role in nutrient homeostasis, enhancing nutrient assimilation through enhanced gastrointestinal function, as well as increasing nutrient disposal. Stimulates intestinal glucose transport and decreases

Search completed: December 6, 2005, 10:41:51  
Job time : 181.906 secs

```
CC mucosal permeability (By similarity).
CC -!- FUNCTION: Oxyntomodulin significantly reduces food intake (By
CC similarity).
CC -!- FUNCTION: Glucagon may modulate gastric acid secretion and
CC gastro-pyloro-duodenal activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Glucagon is secreted in the A cells of the
CC islets of Langerhans. GLP-1, GLP-2, oxyntomodulin and glicentin
CC are secreted from enteroendocrine cells throughout the
CC gastrointestinal tract. GLP1 and GLP2 are also secreted in
CC selected neurons in the brain.
CC -!- INDUCTION: Glucagon release is stimulated by hypoglycemia and
CC inhibited by hyperglycemia, insulin, and somatostatin. GLP-1 and
CC GLP-2 are induced in response to nutrient ingestion (By
CC similarity).
CC -!- PTM: Proglucagon is posttranslationally processed in a tissue-
CC specific manner in pancreatic A cells and intestinal L cells. In
CC pancreatic A cells, the major bioactive hormone is glucagon
CC cleaved by PCSK2/PC2. In the intestinal L cells PCSK1/PC1
CC liberates GLP-1, GLP-2, glicentin and oxyntomodulin. GLP-1 is
CC further N-terminally truncated by posttranslational processing in
CC the intestinal L cells resulting in GLP-1(7-37) GLP-1-(7-36)amide.
CC The C-terminal amidation is neither important for the metabolism
CC of GLP-1 nor for its effects on the endocrine pancreas (By
CC similarity).
CC -!- SIMILARITY: Belongs to the glucagon family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC -----
CC EMBL; AF308439; AAL09425.1; -; mRNA.
CC PIR; A60318; GCDG69.
CC HSSP; P01274; 1GCN.
CC Ensembl; ENSCARG0000010414; Canis familiaris.
CC InterPro; IPR000532; Glucagon.
CC Pfam; PF00123; Hormone 2; 3.
CC PRINTS; PR00275; GLUCAGON.
CC SMART; SM00070; GLUCA; 3.
CC DR PROSITE; PS00260; GLUCAGON; 4.
CC Amidation; Cleavage on pair of basic residues;
CC Direct protein sequencing; Glucagon family; Hormone; Signal.
FT SIGNAL 1 20
FT PEPTIDE 21 89 Glicentin.
FT PEPTIDE 21 50 Glicentin-related polypeptide (By
FT similarity).
FT PEPTIDE 53 89 Oxyntomodulin (By similarity).
FT PEPTIDE 53 81 Glucagon (By similarity).
FT PROPEP 84 89 By similarity.
FT PEPTIDE 92 128 Glucagon-like peptide 1.
FT PEPTIDE 98 128 Glucagon-like peptide 1(7-37).
FT PEPTIDE 98 127 Glucagon-like peptide 1(7-36).
FT PROPEP 131 145 By similarity.
FT PEPTIDE 146 178 Glucagon-like peptide 2 (By similarity).
FT SITE 52 53 Cleavage (by PCSK2).
FT SITE 83 84 Cleavage (by PCSK1 and PCSK2).
FT SITE 91 92 Cleavage (by PCSK1).
FT SITE 97 98 Cleavage (by PCSK1).
FT SITE 130 131 Cleavage (by PCSK1).
FT SITE 145 146 Cleavage (by PCSK1).
FT MOD_RES 127 127 Arginine amide (G-128 provides amide
FT group) (By similarity).
FT SEQUENCE 180 AA; 21115 MW; 80F66941AFC324FD CRC64;
Query Match 16.6%; Score 157; DB 1; Length 180;
Best Local Similarity 96.8%; Pred. No. 8.4e-06;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 HGEFTFTSDVSSYLEGQAQKEFTIAVLVKGKRG 32
Db 98 HAEGTFTSDVSSYLEGQAQKEFTIAVLVKGKRG 128
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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:12 ; Search time 29.4355 Seconds  
(without alignments)  
575.296 Million cell updates/sec

Title: US-10-611-655-10  
Perfect score: 944  
Sequence: 1 MHGEGTFTSDVSSYLEGQAA.....VKCEGISLLAQTSHHHHH 176

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: Pirl.\*  
2: Pirl.\*  
3: Pirl.\*  
4: Pirl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	67.5	161	1 TDHU	Thy-1 membrane gly
2	630	66.7	161	2 T47130	hypothetical prote
3	421	44.6	161	1 TDRT	Thy-1 membrane gly
4	406.5	43.1	162	1 TDMS	Thy-1 membrane gly
5	305.5	32.4	160	2 A48975	Thy-1 glycoprotein
6	157	16.6	158	1 GCPG	glucagon precursor
7	157	16.6	180	1 GCHY	glucagon precursor
8	157	16.6	180	1 GCHY	glucagon precursor
9	157	16.6	180	1 GCGP	glucagon precursor
10	157	16.6	180	1 GCHU	glucagon precursor
11	157	16.6	180	1 GCRT	glucagon precursor
12	157	16.6	180	1 GCRTDU	glucagon precursor
13	157	16.6	180	2 A57294	glucagon precursor
14	145	15.4	151	1 GCCH	glucagon precursor
15	145	15.4	206	2 I51301	proglucagon - chic
16	127	13.5	268	2 A56446	lg heavy chain V r
17	125	13.2	101	1 GCFGB	glucagon precursor
18	122	12.9	30	2 C61125	glucagon-like pept
19	122	12.9	30	2 B61125	glucagon-like pept
20	122	12.9	122	1 GCAF2	Glucagon 2 precurs
21	114	12.1	66	2 I51093	glucagon - chinook
22	114	12.1	178	2 I51058	glucagon I precurs
23	113	12.0	63	1 GCIDC	glucagon precursor
24	112	11.9	72	1 GCGXA	glucagon precursor
25	112	11.9	411	2 I58156	Brn-3.2 - mouse
26	109.5	11.6	410	2 I38502	gene Brn-3b protei
27	109	11.5	60	1 GCQNC	glucagon precursor
28	109	11.5	178	2 I51057	glucagon II precur
29	107	11.3	30	2 S44473	glucagon-like pept

30	99.5	10.5	39	1 HWCH4G	exendin-4 - Gila m
31	99	10.5	87	1 GCFIS	glucagon precursor
32	98.5	10.4	2783	1 A41948	alpha-fetoprotein
33	96.5	10.2	124	1 GCAF	glucagon 1 precurs
34	96	10.2	29	2 S07211	glucagon - marbled
35	95.5	10.1	1022	2 T17405	developmental prot
36	95	10.1	31	2 S44472	glucagon G2 - Nort
37	95	10.1	877	2 T43449	hypothetical prote
38	94.5	10.0	160	2 H88114	protein F53C3.6 [l
39	94	10.0	29	1 GCDP	glucagon - smaller
40	93	9.9	31	2 S44471	glucagon G1 - Nort
41	92.5	9.8	239	2 S49193	GCR 101 protein -
42	92.5	9.8	249	2 S41374	single chain Fv an
43	92	9.7	29	1 GCEN	glucagon - elephan
44	92	9.7	508	2 S59870	fork head domain p
45	92	9.7	1093	2 I38533	AF17 protein - hum

ALIGNMENTS

RESULT 1

TDHU

Thy-1 membrane glycoprotein precursor - human  
N/Alternate names: Thy-1 antigen  
C/Species: Homo sapiens (man)  
C/Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 09-Jul-2004  
C/Accession: A02106  
R;Seki, T.; Spurr, N.; Obata, F.; Goyert, S.; Goodfellow, P.; Silver, J.  
Proc. Natl. Acad. Sci. U.S.A. 82, 6657-6661, 1985  
A/Title: The human Thy-1 gene: structure and chromosomal location.  
A/Reference number: A02106; MUID:86016759; PMID:2864690  
A/Accession: A02106  
A/Molecule type: DNA  
A/Residues: 1-161 <SEK>  
A/Cross-references: UNIPROT:P04216; UNIPARC:UPI0000049811; GB:M11749; NID:G339682; PIDN  
C/Genetics:  
A/Gene: GDB:THY1  
A/Cross-references: GDB:119614; OMIM:188230  
A/Map position: 11q22.3-11q23  
A/Introns: 13/1; 125/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: glycoprotein; thymocyte; transmembrane protein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-161/Product: Thy-1 membrane glycoprotein #status predicted <MAT>  
F;20-141/Domain: extracellular #status predicted <EX1>  
F;31-106/Domain: immunoglobulin homology <IMM>  
F;142-161/Domain: transmembrane #status predicted <TMW>  
F;42,119,139/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.5%; Score 637; DB 1; Length 161;  
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Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 49 QKVTSLTACLDVDSLDCHRENTSSSPQYSESLFRETREYKXVLFGTGVPEHTYRSRTN 108

Db 20 QKVTSLTACLDVDSLDCHRENTSSSPQYSESLFRETREYKXVLFGTGVPEHTYRSRTN 79

Qy 109 FTSKYHMKVLYLSAFTSKDEGTVCALHSHGSHPPISQNVTVLRDKLVKCEGISLLAQN 168

Db 80 FTSKYHMKVLYLSAFTSKDEGTVCALHSHGSHPPISQNVTVLRDKLVKCEGISLLAQN 139

Qy 169 TS 170

Db 140 TS 141

RESULT 2

T47130

hypothetical protein DKFZp761B15121.1 - human  
C/Species: Homo sapiens (man)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C/Accession: T47130

R; Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Weil, B.; Wiemann, S.  
submitted to the Protein Sequence Database, March 2000  
A;Reference number: Z24374  
A;Accession: T47130  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-161 <AAA>  
A;Cross-references: UNIPROT:P04216; UNIPARC:UPI0000136F1P; EMBL:AL161958  
A;Experimental source: adult amygdala; clone DKFZp761B15121  
C;Genetics:  
A;Note: DKFZp761B15121.1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 66.7%; Score 630; DB 2; Length 161;  
Best Local Similarity 99.2%; Pred. No. 1.5e-47;  
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 49 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRTKKHVLFGTGVGPETHYRSRTN 108  
Db 20 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRTKKHVLFGTGVGPETHYRSRTN 79  
  
QY 109 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRLDKLVKCGISLLAQN 168  
Db 80 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRLDKLVKCGISLLAQN 139  
  
QY 169 TS 170  
Db 140 TS 141

RESULT 3  
TDRT  
thy-1 membrane glycoprotein precursor - rat  
N;Alternate names: thy-1 antigen  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 29-Jun-1981 #sequence revision 08-Feb-1996 #text change 09-Jul-2004  
C;Accession: B45909; A45909; A25255; A21652; A90311; A93296; A02107  
R;Seki, T.; Moriuchi, T.; Chang, H.C.; Denome, R.; Silver, J.  
Nature 313, 485-487, 1985  
A;Title: Structural organization of the rat thy-1 gene.  
A;Reference number: A45909; MUID:851111162; PMID:2857477  
A;Accession: B45909  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-161 <SEK>  
A;Cross-references: UNIPROT:P01830; UNIPARC:UPI0000136F21; GB:X02002; NID:g57363; PIDN:C  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 20-161 <SE2>  
A;Cross-references: UNIPARC:UPI0000170B3F  
R;Seki, T.; Chang, H.C.; Moriuchi, T.; Denome, R.; Silver, J.  
Fed. Proc. 44, 2865-2869, 1985  
A;Title: Thy-1: a hydrophobic transmembrane segment at the carboxyl terminus.  
A;Reference number: A25255; MUID:86005549; PMID:2864289  
A;Accession: A25255  
A;Molecule type: DNA  
A;Residues: 1-70, 'Q', 72-161 <SE3>  
A;Cross-references: UNIPARC:UPI0000170B3E; GB:X03152; NID:g57357; PIDN:CAA26931.1; PID:g  
R;Moriuchi, T.; Silver, J.  
FEBS Lett. 178, 105-107, 1984  
A;Title: Rat Thy-1 antigen has a hydrophobic segment at the carboxyl terminus.  
A;Reference number: A21652; MUID:85051865; PMID:6149956  
A;Accession: A21652  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 20-161 <MOR>  
A;Cross-references: UNIPARC:UPI0000170B3F; GB:X03150; GB:J00792; GB:X01445  
R;Campbell, D.G.; Gagnon, J.; Reid, K.B.M.; Williams, A.F.  
Biochem. J. 195, 15-30, 1981  
A;Title: Rat brain Thy-1 glycoprotein. The amino acid sequence, disulphide bonds and an  
A;Reference number: A90311; MUID:82068190; PMID:6118137  
A;Accession: A90311

A;Molecule type: protein  
A;Residues: 20-130 <CAM>  
A;Cross-references: UNIPARC:UPI0000173743  
A;Note: this sequence shows homologies with immunoglobulin domains  
R;Moriuchi, T.; Chang, H.C.; Denome, R.; Silver, J.  
Nature 301, 80-82, 1983  
A;Title: Thy-1 cDNA sequence suggests a novel regulatory mechanism.  
A;Reference number: A93296; MUID:83115223; PMID:6130472  
A;Accession: A93296  
A;Molecule type: mRNA  
A;Residues: 1-122 <MO2>  
A;Cross-references: UNIPARC:UPI0000173744  
C;Comment: This glycoprotein is a major constituent of brain-cell membrane and is abunda  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: glycoprotein; membrane protein; pyroglutamic acid  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-130/Product: thy-1 membrane glycoprotein #status experimental <MAT>  
F;31-106/Domain: immunoglobulin homology <IMM>  
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer  
F;28-130,38-104/Disulfide bonds: #status experimental  
F;42,93,117/Binding site: carbohydate (Asn) (covalent) #status experimental  
  
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Best Local Similarity 67.2%; Pred. No. 1.9e-29;  
Matches 82; Conservative 15; Mismatches 25; Indels 0; Gaps 0;  
  
QY 49 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRTKKHVLFGTGVGPETHYRSRTN 108  
Db 20 QKVTSLTACLVDSRLDCRHSNTSSPIQYEFSLTRTKKHVLFGTGVGPETHYRSRTN 79  
  
QY 109 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRLDKLVKCGISLLAQN 168  
Db 80 LFSDFRIKVTLANFTTKDGYMCELRSVGNQNTSSNKTINIVIRDKLVKCGISLLVQN 139  
  
QY 169 TS 170  
Db 140 TS 141  
  
RESULT 4  
TMS  
Thy-1 membrane glycoprotein precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jul-1982 #sequence revision 28-May-1986 #text change 09-Jul-2004  
C;Accession: A94278; A24647; A94265; I5928; I55957; A02108  
R;Seki, T.; Chang, H.C.; Moriuchi, T.; Denome, R.; Floegh, H.; Silver, J.  
Science 227, 649-651, 1985  
A;Title: A hydrophobic transmembrane segment at the carboxyl terminus of Thy-1.  
A;Reference number: A94278; MUID:85115360; PMID:2857501  
A;Accession: A94278  
A;Molecule type: DNA  
A;Residues: 1-162 <SEK>  
A;Cross-references: UNIPROT:P01831; UNIPARC:UPI000002395E; GB:M10246; NID:g202032; PIDN:  
R;Giguere, V.; Isobe, K.I.; Grosveld, F.  
EMBO J. 4, 2017-2024, 1985  
A;Title: Structure of the murine Thy-1 gene.  
A;Reference number: A24647; MUID:86055760; PMID:2866091  
A;Contents: Thy-1.2 allotype  
A;Accession: A24647  
A;Molecule type: DNA  
A;Residues: 1-162 <GIG>  
A;Cross-references: UNIPARC:UPI000002395E  
A;Experimental source: strain BALB/c  
R;Williams, A.F.; Gagnon, J.  
Science 216, 696-703, 1982  
A;Title: Neuronal cell Thy-1 glycoprotein: homology with immunoglobulin.  
A;Reference number: A94265; MUID:82199396; PMID:6177036  
A;Accession: A94265  
A;Molecule type: protein  
A;Residues: 20-131 <WIL>  
A;Cross-references: UNIPARC:UPI0000173745  
A;Note: the Thy-1.1 sequence differs from that shown in having 108-Arg  
R;Chang, H.

Proc. Natl. Acad. Sci. U.S.A. 82, 3819-3823, 1985  
A;Title: Isolation and characterization of mouse Thy-1 genomic clones.  
A;Reference number: I59028; MUID:85216593; PMID:2582427  
A;Accession: I59028  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-162 <RES>  
A;Cross-references: UNIPARC:UPI00002395E; GB:M11160; NID:G202034; PIDN:AAA40441.1; PID:  
R;Ingraham, H.A.; Lawless, G.M.; Evans, G.A.  
J. Immunol. 136, 1482-1489, 1986  
A;Title: The mouse Thy-1.2 glycoprotein gene: Complete sequence and identification of an  
A;Reference number: I55957; MUID:86113437; PMID:2868059  
A;Accession: I55957  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-162 <RES>  
A;Cross-references: UNIPARC:UPI00002395E; GB:M12379; NID:G202040; PIDN:AAA40443.1; PID:  
C;Comment: The Thy-1.2 sequence is shown.  
C;Genetics:  
A;Map position: 9  
A;Introns: 13/1; 126/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: glycoprotein; pyroglytamic acid; T-cell; transmembrane protein  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-162/Product: Thy-1 membrane glycoprotein #status predicted <MAT>  
F;31-107/Domain: immunoglobulin homology <IMW>  
F;143-162/Domain: transmembrane #status predicted <TMW>  
F;20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen  
F;28-131,38-105/Disulfide bonds: #status experimental  
F;42,94,118/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 43.1%; Score 406.5; DB 1; Length 162;  
Best Local Similarity 65.0%; Pred. No. 3.4e-28;  
Matches 80; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

Qy 49 QKVTSLTACLVDSLRDCHHE-NTSSSPLOYEFSFTRETKKHLVFGTVGVPEHTYRSRT 107  
Db 20 QKVTSLTACLVNQNLDRCHENNTDINSIOHEFSLTREKKRHLVSGTLGIPHTYRSRV 79

Qy 108 NFTSKYHKVLYLSAFTSKDEGTYTCALHSHSGSPPISSONVTVLRLDKLVKCGISLLAQ 167  
Db 80 TLSNQPIKVLTLANFTTKDEGDFCELVSGANPMSNKSISVYRDLKLVKCGISLLVQ 139

Qy 168 NTS 170  
Db 140 NTS 142

RESULT 5  
A48975  
Thy-1 glycoprotein - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A48975  
R;Dowsing, B.J.; Gooley, A.A.; Gunning, P.; Cunningham, A.; Jeffrey, P.L.  
Brain Res. Mol. Brain Res. 14, 250-260, 1992  
A;Title: Molecular cloning and primary structure of the avian Thy-1 glycoprotein.  
A;Reference number: A48975; MUID:93061794; PMID:1359371  
A;Accession: A48975  
A;Status: preliminary  
A;Molecule type: mRNA; protein  
A;Residues: 1-160 <DOM>  
A;Cross-references: UNIPROT:Q07212; UNIPARC:UPI0000136F1D; GB:L14924; NID:G289826; PIDN:  
A;Note: sequence extracted from NCBI backbone (NCBIN:117489, NCBIPI:117490)  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: glycoprotein

Query Match 32.4%; Score 305.5; DB 2; Length 160;  
Best Local Similarity 48.4%; Pred. No. 1.9e-19;  
Matches 59; Conservative 25; Mismatches 37; Indels 1; Gaps 1;

Qy 49 QKVTSLTACLVDSLRDCHRENTSSSPIOQEFSLTRETKKHLVFGTVGVPEHTYRSRTN 108

Db 20 QMIRDSACLLQSLRVDCRVENKTSNPLTYEFSLTRQ-QKHIIOSTISVSENVTNRAN 78  
Qy 109 FTSKYHKVLYLSAFTSKDEGTYTCALHSHSGSPPISSONVTVLRLDKLVKCGISLLAQ 168  
Db 79 VTMKHLVCLYLSHFTTSDEGYMCELKATNDYTGQIKNTIVIKDLKCKVRLSLLQN 138  
Qy 169 TS 170  
Db 139 TS 140

RESULT 6  
GCPG  
glucagon precursor - pig (fragment)  
N;Alternate names: glicentin; oxyntomodulin  
N;Contains: glicentin-related peptide; glucagon; glucagon-37 (oxyntomodulin); glucagon-  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 17-Dec-1982 #sequence\_revision 31-Mar-1993 #text\_change 20-Mar-1998  
C;Accession: A01540; A60312; A91781; B32614; A28064  
R;Thim, L.; Moody, A.J.  
Regul. Pept. 2, 139-150, 1981  
A;Title: The primary structure of porcine glicentin (proglucagon).  
A;Reference number: A94233; MUID:81248172; PMID:6894800  
A;Accession: A01540  
A;Molecule type: protein  
A;Residues: 1-69 <TH1>  
A;Cross-references: UNIPARC:UPI0000173500  
R;Thim, L.; Moody, A.J.  
Regul. Pept. Suppl. 2, S33, 1983  
A;Title: Primary structure of a possible porcine proglucagon fragment.  
A;Reference number: A60312  
A;Accession: A60312  
A;Molecule type: protein  
A;Residues: 1-30 <TH2>  
A;Cross-references: UNIPARC:UPI000002C9AC  
A;Note: this peptide is co-secreted with glucagon from the pancreas  
R;Bromer, W.W.; Sinn, L.G.; Behrens, O.K.  
J. Am. Chem. Soc. 79, 2807-2810, 1957  
A;Title: The amino acid sequence of glucagon. V. Location of amide groups, acid degrada  
A;Reference number: A91781  
A;Accession: A91781  
A;Molecule type: protein  
A;Residues: 33-61 <BRO>  
A;Cross-references: UNIPARC:UPI000002C586  
R;Orskov, C.; Bersani, M.; Johnsen, A.H.; Hojrup, P.; Holst, J.J.  
J. Biol. Chem. 264, 12826-12829, 1989  
A;Title: Complete sequences of glucagon-like peptide-1 from human and pig small intestine.  
A;Reference number: A92732; MUID:89327238; PMID:2753890  
A;Accession: B32614  
A;Molecule type: protein  
A;Residues: 78-107 <ORS>  
A;Cross-references: UNIPARC:UPI0000032E2A  
R;Buhl, T.; Thim, L.; Kofod, H.; Orskov, C.; Harling, H.; Holst, J.J.  
J. Biol. Chem. 263, 8621-8624, 1988  
A;Title: Naturally occurring products of proglucagon 111-160 in the porcine and human s  
A;Reference number: A28064; MUID:88243712; PMID:3379036  
A;Accession: A28064  
A;Molecule type: protein  
A;Residues: 111-158 <BUH>  
A;Cross-references: UNIPARC:UPI0000173501  
C;Comment: X's represent missing amino acids, mostly basic, that are predicted to exist  
C;Superfamily: glucagon  
C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; interes  
F;1-69/Product: glucagon-69 #status experimental <G69>  
F;1-30/Region: glicentin-related peptide #status experimental  
F;33-69/Product: glucagon-37 #status predicted <G37>  
F;33-61/Product: glucagon #status experimental <GCN>  
F;78-107/Product: glucagon-like peptide 1 #status experimental <GL1>  
F;126-158/Product: glucagon-like peptide 2 #status experimental <GL2>  
F;107/Modified site: amidated carboxyl end (Arg) (amide in mature form from following g

Query Match 16.6%; Score 157; DB 1; Length 158;  
Best Local Similarity 96.8%; Pred. No. 1.4e-06;



A;Title: Structure of the human glucagon gene.  
A;Reference number: A24377; MUID:86259053; PMID:3725587  
A;Accession: A24377  
A;Molecule type: DNA  
A;Residues: 1-180 <WHI>  
A;Cross-references: UNIPARC:P01275; UNIPARC:UPI000012B832; GB:X03991  
R;Bell, G.I.; Sanchez-Pescador, R.; Laybourn, P.J.; Najarian, R.C.  
Nature 304, 368-371, 1983  
A;Title: Exon duplication and divergence in the human preproglucagon gene.  
A;Reference number: A44197; MUID:83271477; PMID:6877358  
A;Accession: A44197  
A;Molecule type: DNA  
A;Residues: 1-179 <BEL>  
A;Cross-references: UNIPARC:UPI000016A9A7; GB:V01515; PIDN:CAA24759.1; PID:9  
R;Drucker, D.J.; Aea, S.  
J. Biol. Chem. 263, 13475-13478, 1988  
A;Title: Glucagon gene expression in vertebrate brain.  
A;Reference number: A30875; MUID:88330860; PMID:2901414  
A;Accession: A30875  
A;Molecule type: mRNA  
A;Residues: 1-180 <DRU>  
A;Cross-references: UNIPARC:UPI000012B832; GB:J04040; NID:G183269; PIDN:AAA52567.1; PID:  
R;Orskov, C.; Bersani, M.; Johnsen, A.H.; Hojrup, P.; Holst, J.J.  
J. Biol. Chem. 264, 12826-12829, 1989  
A;Title: Complete sequences of glucagon-like peptide-1 from human and pig small intestine  
A;Reference number: A92732; MUID:89327238; PMID:2753690  
A;Accession: A32614  
A;Molecule type: protein  
A;Residues: 98-127 <ORS>  
A;Cross-references: UNIPARC:UPI0000032E2A  
R;Thomsen, J.; Kristiansen, K.; Brumfeldt, K.; Sundby, F.  
FEBS Lett. 21, 315-319, 1972  
A;Title: The amino acid sequence of human glucagon.  
A;Reference number: A91373  
A;Accession: A01541  
A;Molecule type: protein  
A;Residues: 53-81 <THO>  
A;Cross-references: UNIPARC:UPI000002C586  
R;Tsugita, A.; Takamoto, K.; Kamo, M.; Iwade, H.  
Eur. J. Biochem. 206, 691-696, 1992  
A;Title: C-terminal sequencing of protein. A novel partial acid hydrolysis and analysis  
A;Reference number: S23188; MUID:92298996; PMID:1606956  
A;Accession: S23309  
A;Molecule type: protein  
A;Residues: 53-81 <TSU>  
A;Cross-references: UNIPARC:UPI000002C586  
C;Comment: In pancreatic alpha-cells, proglucagon is processed to glucicentin-related poly  
ptinal L cells, proglucagon is processed to truncated glucagon-like peptide 1, glucagon-  
C;Genetics:  
A;Gene: GDB:GCG  
A;Cross-references: GDB:119265; OMIM:138030  
A;Map position: 2q36-2q37  
A;Introns: 31/2; 85/2; 131/2; 179/2  
C;Superfamily: glucagon  
C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; intest  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-180/Product: proglucagon #status experimental <PGC>  
F;21-89/Product: glucicentin #status experimental <GLN>  
F;53-89/Product: oxyntomodulin #status experimental <OXN>  
F;53-81/Product: glucagon #status experimental <GCN>  
F;92-178/Product: major proglucagon fragment #status experimental <MPGF>  
F;92-127/Product: glucagon-like peptide 1 #status experimental <GL1>  
F;98-127/Product: truncated glucagon-like peptide 1 #status experimental <TGL>  
F;146-178/Product: glucagon-like peptide 2 #status predicted <GL2>  
F;127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl  
Query Match 16.6%; Score 157; DB 1; Length 180;  
Best Local Similarity 96.8%; Pred. No. 1.6e-06;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 HSGGTFTSDVSSYLEGQAAKEFTIAWLKGRG 32

DB 98 HAEGTFTSDVSSYLEGQAAKEFTIAWLKGRG 128  
RESULT 11  
GCRDTU  
Glucagon precursor - rat  
N;Contains: glucicentin-related peptide; glucagon; glucagon-like peptide 1; glucagon-like  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1987 #sequence revision 30-Sep-1987 #text\_change 09-Jul-2004  
C;Accession: A22655; A25190; A44198  
R;Heinrich, G.; Gros, P.; Habener, J.F.  
J. Biol. Chem. 259, 14082-14087, 1984  
A;Title: Glucagon gene sequence: four of six exons encode separate functional domains o  
A;Reference number: A22655; MUID:85054853; PMID:6094539  
A;Accession: A22655  
A;Molecule type: DNA  
A;Residues: 1-180 <HEI>  
A;Cross-references: UNIPROT:P06883; UNIPARC:UPI000002DB13; EMBL:K02809  
A;Note: the authors translated the codon TTG for residue 10 as Glu and ACC for residue  
R;Mojsos, S.; Heinrich, G.; Wilson, I.B.; Ravazzola, M.; Orci, L.; Habener, J.F.  
J. Biol. Chem. 261, 11880-11889, 1986  
A;Title: Preproglucagon gene expression in pancreas and intestine diversifies at the le  
A;Reference number: A25190; MUID:86304324; PMID:3528148  
A;Accession: A25190  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-180 <MOJ>  
A;Cross-references: UNIPARC:UPI000002DB13  
R;Heinrich, G.; Gros, P.; Lund, P.K.; Bentley, R.C.; Habener, J.F.  
Endocrinology 115, 2176-2181, 1984  
A;Title: Pre-proglucagon messenger ribonucleic acid: nucleotide and encoded amino acid  
A;Reference number: A44198; MUID:85051023; PMID:6548696  
A;Accession: A44198  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-180 <HE2>  
A;Cross-references: UNIPARC:UPI000002DB13; GB:K02809; GB:K02810; GB:K02811; GB:K02812  
C;Genetics:  
A;Introns: 31/2; 85/2; 131/2; 179/2  
C;Superfamily: glucagon  
C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancr  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-180/Product: proglucagon #status predicted <PGC>  
F;21-50/Region: glucicentin-related peptide #status predicted  
F;53-81/Product: glucagon #status predicted <GCN>  
F;98-127/Product: glucagon-like peptide 1 #status predicted <GL1>  
F;146-180/Product: glucagon-like peptide 2 #status predicted <GL2>  
F;127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following g  
Query Match 16.6%; Score 157; DB 1; Length 180;  
Best Local Similarity 96.8%; Pred. No. 1.6e-06;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 HSGGTFTSDVSSYLEGQAAKEFTIAWLKGRG 32  
DB 98 HAEGTFTSDVSSYLEGQAAKEFTIAWLKGRG 128  
RESULT 12  
GCRDTU  
Glucagon precursor - degu  
N;Contains: glucicentin-related peptide; glucagon; glucagon-like peptide 1; glucagon-like  
C;Species: Octodon degus (degu)  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: C36118  
R;Nishi, M.; Steiner, D.F.  
Mol. Endocrinol. 4, 1192-1198, 1990  
A;Title: Cloning of complementary DNAs encoding islet amyloid polypeptide, insulin, and  
A;Reference number: A36118; MUID:91155952; PMID:2293024  
A;Accession: C36118  
A;Molecule type: mRNA  
A;Residues: 1-180 <NIS>

A;Cross-references: UNIPROT:P22890; UNIPARC:UIPI000012B839; GB:M57688; NID:g202467; PIDN:  
C;Superfamily: glucagon  
C;Keywords: amidated carboxyl end; carbohydrate metabolism; duplication; hormone; pancre  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-180/Product: proglucagon #status predicted <PGC>  
F;21-50/Region: gliadin-related peptide #status predicted  
F;53-81/Product: glucagon #status predicted <GCN>  
F;98-127/Product: glucagon-like peptide 1 #status predicted <GLI>  
F;146-178/Product: glucagon-like peptide 2 #status predicted <GL2>  
F;127/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gl

Query Match 16.6%; Score 157; DB 1; Length 180;  
Best Local Similarity 96.8%; Pred. No. 1.6e-06;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HGEGTFSDVSSYLEGGQAQAEFIANLVKGRG 32  
| | | | | | | | | | | | | | | | | |  
Db 98 HAEGTFTSDVSSYLEGGQAQAEFIANLVKGRG 128

RESULT 13  
A57294  
glucagon precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 01-Dec-1995 #sequence\_revision 01-Dec-1995 #text\_change 09-Jul-2004  
R;Accession: A57294; S49903  
R;Rothenberg, M.E.; Eilertson, C.D.; Klein, K.; Zhou, Y.; Lindberg, I.; McDonald, J.K.;  
J. Biol. Chem. 270, 10136-10146, 1995  
A;Title: Processing of mouse proglucagon by recombinant prohormone convertase 1 and immu  
A;Reference number: A57294; MUID:95247722; PMID:7730317  
A;Accession: A57294  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-180 <ROT>  
A;Cross-references: UNIPROT:P55095; UNIPARC:UIPI000000192D; EMBL:Z46845; NID:g599880; PIDN:  
C;Superfamily: glucagon  
C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

Query Match 16.6%; Score 157; DB 2; Length 180;  
Best Local Similarity 96.8%; Pred. No. 1.6e-06;  
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HGEGTFSDVSSYLEGGQAQAEFIANLVKGRG 32  
| | | | | | | | | | | | | | | | | |  
Db 98 HAEGTFTSDVSSYLEGGQAQAEFIANLVKGRG 128

RESULT 14  
GCCH  
glucagon precursor - chicken  
N;Contains: glucagon; glucagon-like peptide 1  
C;Species: Gallus gallus (chicken)  
C;Date: 31-Dec-1991 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: S09992; A92189; A60836; A01542  
R;Haegawa, S.; Terazono, K.; Nata, K.; Takada, T.; Yamamoto, H.; Okamoto, H.  
FEBS Lett. 264, 117-120, 1990  
A;Title: Nucleotide sequence determination of chicken glucagon precursor cDNA. Chicken F  
A;Reference number: S09992; MUID:90249492; PMID:2338135  
A;Accession: S09992  
A;Molecule type: mRNA  
A;Residues: 1-151 <HAS>  
A;Cross-references: UNIPROT:P01277; UNIPARC:UIPI000002AA99; EMBL:Y07539; NID:g63749; PIDN:  
R;Pollock, H.G.; Kimmel, J.R.  
J. Biol. Chem. 250, 9377-9380, 1975  
A;Title: Chicken glucagon. Isolation and amino acid sequence studies.  
A;Reference number: A92189; MUID:76069271; PMID:1194290  
A;Accession: A92189  
A;Molecule type: protein  
A;Residues: 55-83 <POL>  
A;Cross-references: UNIPARC:UIPI000012B830  
R;Huang, J.; Eng, J.; Yalow, R.S.  
Horm. Metab. Res. 19, 542-544, 1987  
A;Title: Chicken glucagon: sequence and potency in receptor assay.

Result No.	Score	Query Match	Length	DB	ID	Description
1	630	66.7	161	2	US-09-949-016-11168	Sequence 11168, A
2	387	41.0	105	2	US-09-513-999C-4247	Sequence 4247, Ap
3	174	18.4	176	1	US-08-835-231-18	Sequence 18, Appl
4	174	18.4	176	2	US-09-108-661-18	Sequence 18, Appl
5	163	17.3	31	2	US-09-209-799D-16	Sequence 16, Appl
6	163	17.3	31	2	US-09-614-847-113	Sequence 123, App
7	163	17.3	31	2	US-09-997-792A-14	Sequence 14, Appl
8	163	17.3	32	2	US-09-614-847-147	Sequence 147, App
9	163	17.3	37	2	US-09-614-847-132	Sequence 132, App
10	160	16.9	31	2	US-09-258-750-14	Sequence 14, Appl
11	160	16.9	31	2	US-09-258-750-15	Sequence 15, Appl
12	160	16.9	31	2	US-09-258-750-16	Sequence 16, Appl
13	160	16.9	31	2	US-09-209-799D-28	Sequence 28, Appl
14	160	16.9	31	2	US-09-398-111-14	Sequence 14, Appl
15	160	16.9	31	2	US-09-398-111-15	Sequence 15, Appl
16	160	16.9	31	2	US-09-398-111-16	Sequence 16, Appl
17	160	16.9	31	2	US-09-997-792A-25	Sequence 25, Appl
18	160	16.9	32	2	US-09-258-750-95	Sequence 95, Appl
19	160	16.9	32	2	US-09-398-111-95	Sequence 95, Appl
20	160	16.9	33	2	US-09-258-750-22	Sequence 22, Appl
21	160	16.9	33	2	US-09-398-111-22	Sequence 22, Appl
22	160	16.9	34	2	US-09-258-750-23	Sequence 23, Appl
23	160	16.9	34	2	US-09-398-111-23	Sequence 23, Appl
24	157	16.6	30	2	US-09-209-799D-15	Sequence 15, Appl
25	157	16.6	30	2	US-09-614-847-87	Sequence 87, Appl
26	157	16.6	30	2	US-09-614-847-112	Sequence 112, App
27	157	16.6	30	2	US-09-614-847-113	Sequence 113, App

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; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4247
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; OTHER INFORMATION: score 11.7
; OTHER INFORMATION: seq IALLTLVLQVSRG/QK
US-09-513-999C-4247

Query Match          41.0%; Score 387; DB 2; Length 105;
Best Local Similarity 87.1%; Pred. No. 1.8e-29;
Matches 74; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVPQSLRLDCRHEHTSSPIQYBFSLSLTRETKKHVLFQTVGVPEHTYRSRTN 108
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Db 20 QKVTSLTACLVPQSLRLDCRHEHTSSPIQYBFSLSLTRETKKHVLFQTVGVPEHTYRSRTN 79

QY 109 FTSKYMVKVLYLSAFTSKDEGYTC 133
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Db 80 FTSKYMVKVLYLSASLARTRALHVC 104

RESULT 3
US-08-835-231-18
; Sequence 18, Application US/08835231
; Patent No. 5861284
; GENERAL INFORMATION:
; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 5861284uyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,231
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 18:
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; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-835-231-18

Query Match          18.4%; Score 174; DB 1; Length 176;
Best Local Similarity 76.6%; Pred. No. 6.4e-09;
Matches 36; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 1 MHGEGTFTSDVSSYLEGQAAKEFTIAWLVKRG----GGGGGGGGGEF 43
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Db 1 MHAEGTFTSDVSSYLEGQAAKEFTIAWLVKRGCPEDGGSGGAPPGHF 47

RESULT 4
US-09-108-661-18
; Sequence 18, Application US/09108661
; Patent No. 6287806
; GENERAL INFORMATION:
; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 6287806uyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,661
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 18:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-09-108-661-18

Query Match      18.4%; Score 174; DB 2; Length 176;
Best Local Similarity 76.6%; Pred. No. 6.4e-09;
Matches 36; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 1 MHGEGTFTSDVSSYLEGQAAKEFIAWLKGRG----GGGGSGGGGGRF 43
Db 1 MHGEGTFTSDVSSYLEGQAAKEFIAWLKGRGCPEDGGSGGPPPGHF 47

RESULT 5
US-09-209-799D-16
; Sequence 16, Application US/09209799D
; Patent No. 6380357
; GENERAL INFORMATION:
; APPLICANT: Hermeling, Ronald
; APPLICANT: Hoffmann, James
; APPLICANT: Narasimhan, Chakravarthy
; TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS
; FILE REFERENCE: X-10242
; CURRENT APPLICATION NUMBER: US/09/209,799D
; CURRENT FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-209-799D-16

Query Match      17.3%; Score 163; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 32
Db 1 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 31

RESULT 6
US-09-614-847-123
; Sequence 123, Application US/09614847
; Patent No. 6528486
; GENERAL INFORMATION:
; APPLICANT: Larsen, Bjarne Due
; APPLICANT: Mikkelsen, Jens Mollgaard
; APPLICANT: Neve, Soren
; TITLE OF INVENTION: NOVEL PEPTIDE AGONISTS OF GLP-1 ACTIVITY
; FILE REFERENCE: 55511(45487)
; CURRENT APPLICATION NUMBER: US/09/614,847
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/143,591
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Lys (palmitoyl)
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Gly8-Glp-1(7-36)-Lys37(palmitoyl) (Human)
US-09-614-847-123

Query Match      17.3%; Score 163; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; OTHER INFORMATION: Description of Artificial Sequence: Gly8-Glp-1(7-37)
US-09-614-847-123

Query Match      17.3%; Score 163; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 32
Db 1 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 31

RESULT 7
US-09-997-792A-14
; Sequence 14, Application US/09997792A
; Patent No. 655521
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Glucagon-Like Peptide-1 Crystals
; FILE REFERENCE: X-10242A
; CURRENT APPLICATION NUMBER: US/09/997,792A
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US 60/069,728
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-997-792A-14

Query Match      17.3%; Score 163; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 32
Db 1 HGEFTFTSDVSSYLEGQAAKEFIAWLKGRG 31

RESULT 8
US-09-614-847-147
; Sequence 147, Application US/09614847
; Patent No. 6528486
; GENERAL INFORMATION:
; APPLICANT: Larsen, Bjarne Due
; APPLICANT: Mikkelsen, Jens Mollgaard
; APPLICANT: Neve, Soren
; TITLE OF INVENTION: NOVEL PEPTIDE AGONISTS OF GLP-1 ACTIVITY
; FILE REFERENCE: 55511(45487)
; CURRENT APPLICATION NUMBER: US/09/614,847
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/143,591
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (32)
; OTHER INFORMATION: Lys (palmitoyl)
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Gly8-Glp-1(7-36)-Lys37(palmitoyl) (Human)
US-09-614-847-147

Query Match      17.3%; Score 163; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.5e-09;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HEGGTFTSDVSSYLEGQAAKEFIAMLVKGRG 32  
Db 1 HEGGTFTSDVSSYLEGQAAKEFIAMLVKGRG 31

RESULT 9  
US-09-614-847-122  
; Sequence 122, Application US/09614847  
; Patent No. 6528486  
; GENERAL INFORMATION:  
; APPLICANT: Larsen, Bjarne Due  
; APPLICANT: Mikkelsen, Jens Mollgaard  
; APPLICANT: Neve, Soren  
; TITLE OF INVENTION: NOVEL PEPTIDE AGONISTS OF GLP-1 ACTIVITY  
; FILE REFERENCE: 55511(45487)  
; CURRENT APPLICATION NUMBER: US/09/614,847  
; CURRENT FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/143,591  
; PRIOR FILING DATE: 1999-07-13  
; NUMBER OF SEQ ID NOS: 153  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 122  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: GLY8-GLP-1(7-37)-Lys6  
US-09-614-847-122

Query Match 17.3%; Score 163; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1e-08;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HEGGTFTSDVSSYLEGQAAKEFIAMLVKGRG 32  
Db 1 HEGGTFTSDVSSYLEGQAAKEFIAMLVKGRG 31

RESULT 10  
US-09-258-750-14  
; Sequence 14, Application US/09258750A  
; Patent No. 6268343  
; GENERAL INFORMATION:  
; APPLICANT: KNUDSEN, LISELOTTE BJRERRE  
; APPLICANT: HUUSFELDT, PER OLAF  
; APPLICANT: NIELSEN, PER FRANKLIN  
; TITLE OF INVENTION: GLP-1 DERIVATIVES  
; FILE REFERENCE: 4790.500  
; CURRENT APPLICATION NUMBER: US/09/258,750A  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 08/918,810  
; EARLIER FILING DATE: 1997-08-26  
; EARLIER APPLICATION NUMBER: 60/035,905  
; EARLIER FILING DATE: 1997-01-24  
; EARLIER APPLICATION NUMBER: 60/036,226  
; EARLIER FILING DATE: 1997-01-25  
; EARLIER APPLICATION NUMBER: 60/036,255  
; EARLIER FILING DATE: 1997-01-24  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutagen  
US-09-258-750-14

Query Match 16.9%; Score 160; DB 2; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.6e-08;

Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HEGGTFTSDVSSYLEGQAAKEFIAMLVKGRG 32  
Db 1 HEGGTFTSDVSSYLEGQAAKEFIAMLVKGRG 31

RESULT 11  
US-09-258-750-15  
; Sequence 15, Application US/09258750A  
; Patent No. 6268343  
; GENERAL INFORMATION:  
; APPLICANT: KNUDSEN, LISELOTTE BJRERRE  
; APPLICANT: HUUSFELDT, PER OLAF  
; APPLICANT: NIELSEN, PER FRANKLIN  
; TITLE OF INVENTION: GLP-1 DERIVATIVES  
; FILE REFERENCE: 4790.500  
; CURRENT APPLICATION NUMBER: US/09/258,750A  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 08/918,810  
; EARLIER FILING DATE: 1997-08-26  
; EARLIER APPLICATION NUMBER: 60/035,905  
; EARLIER FILING DATE: 1997-01-24  
; EARLIER APPLICATION NUMBER: 60/036,226  
; EARLIER FILING DATE: 1997-01-25  
; EARLIER APPLICATION NUMBER: 60/036,255  
; EARLIER FILING DATE: 1997-01-24  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutagen  
US-09-258-750-15

Query Match 16.9%; Score 160; DB 2; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.6e-08;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HEGGTFTSDVSSYLEGQAAKEFIAMLVKGRG 32  
Db 1 HEGGTFTSDVSSYLEGQAAKEFIAMLVKGRG 31

RESULT 12  
US-09-258-750-16  
; Sequence 16, Application US/09258750A  
; Patent No. 6268343  
; GENERAL INFORMATION:  
; APPLICANT: KNUDSEN, LISELOTTE BJRERRE  
; APPLICANT: HUUSFELDT, PER OLAF  
; APPLICANT: NIELSEN, PER FRANKLIN  
; TITLE OF INVENTION: GLP-1 DERIVATIVES  
; FILE REFERENCE: 4790.500  
; CURRENT APPLICATION NUMBER: US/09/258,750A  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 08/918,810  
; EARLIER FILING DATE: 1997-08-26  
; EARLIER APPLICATION NUMBER: 60/035,905  
; EARLIER FILING DATE: 1997-01-24  
; EARLIER APPLICATION NUMBER: 60/036,226  
; EARLIER FILING DATE: 1997-01-25  
; EARLIER APPLICATION NUMBER: 60/036,255  
; EARLIER FILING DATE: 1997-01-24  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutagen  
US-09-258-750-16

Query Match 16.9%; Score 160; DB 2; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.6e-08;

; OTHER INFORMATION: mutagen  
US-09-258-750-16

Query Match 16.9%; Score 160; DB 2; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.6e-08;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 32  
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Db 1 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 31

## RESULT 13

US-09-209-799D-28  
; Sequence 28, Application US/09209799D  
; Patent No. 6380357  
; GENERAL INFORMATION:  
; APPLICANT: Hermeling, Ronald  
; APPLICANT: Hoffmann, James  
; APPLICANT: Narasimhan, Chakravarthy  
; TITLE OF INVENTION: GLUCAGON-LIKE PEPTIDE-1 CRYSTALS  
; FILE REFERENCE: X-10242  
; CURRENT APPLICATION NUMBER: US/09/209,799D  
; CURRENT FILING DATE: 1998-12-11  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 28  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-09-209-799D-28

Query Match 16.9%; Score 160; DB 2; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.6e-08;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 32  
|||||  
Db 1 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 31

## RESULT 14

US-09-398-111-14  
; Sequence 14, Application US/09398111  
; Patent No. 6458924  
; GENERAL INFORMATION:  
; APPLICANT: KNUDSEN, LISELOTTE BJERRE  
; APPLICANT: HUUSFELDT, PER OLAF  
; APPLICANT: NIELSEN, PER FRANKLIN  
; TITLE OF INVENTION: GLP-1 DERIVATIVES  
; FILE REFERENCE: 4790.500  
; CURRENT APPLICATION NUMBER: US/09/398,111  
; CURRENT FILING DATE: 1999-09-16  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/08/918,810A  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,905  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-24  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/036,226  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-25  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/036,255  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-24  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutagen  
US-09-398-111-14

Query Match 16.9%; Score 160; DB 2; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.6e-08;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 32  
|||||  
Db 1 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 31

## RESULT 15

US-09-398-111-15  
; Sequence 15, Application US/09398111  
; Patent No. 6458924  
; GENERAL INFORMATION:  
; APPLICANT: KNUDSEN, LISELOTTE BJERRE  
; APPLICANT: HUUSFELDT, PER OLAF  
; APPLICANT: NIELSEN, PER FRANKLIN  
; TITLE OF INVENTION: GLP-1 DERIVATIVES  
; FILE REFERENCE: 4790.500  
; CURRENT APPLICATION NUMBER: US/09/398,111  
; CURRENT FILING DATE: 1999-09-16  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/08/918,810A  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,905  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-24  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/036,226  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-25  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/036,255  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-24  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mutagen  
US-09-398-111-15

Query Match 16.9%; Score 160; DB 2; Length 31;  
Best Local Similarity 96.8%; Pred. No. 1.6e-08;  
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 32  
|||||  
Db 1 HGEFTSDVSSYLEGQAAKEFTIAWLKGRG 31

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OM protein - protein search, using sw model

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532.965 Million cell updates/sec

Title: US-10-611-655-10  
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Maximum Match 100%

Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pap:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	944	100.0	176	5	US-10-611-655-10
2	787	83.4	334	5	US-10-611-655-6
3	787	83.4	334	5	US-10-611-655-8
4	637	67.5	161	3	US-09-918-715-220
5	637	67.5	161	4	US-10-474-794-220
6	637	67.5	161	5	US-10-979-159-220
7	630	66.7	161	4	US-10-165-603-32
8	630	66.7	161	4	US-10-794-899-66
9	630	66.7	161	5	US-10-287-436A-449
10	630	66.7	161	5	US-10-287-436A-1149
11	630	66.7	165	3	US-09-925-301-1384
12	630	66.7	165	4	US-10-106-698-4624
13	617.5	65.4	162	5	US-10-611-655-1
14	600	63.6	159	4	US-10-322-281-20
15	424	44.9	171	5	US-10-450-763-49897
16	421	44.6	161	4	US-10-165-603-30
17	421	44.6	161	4	US-10-794-899-64
18	406.5	43.1	162	3	US-09-918-715-303
19	406.5	43.1	162	4	US-10-474-794-303
20	406.5	43.1	162	5	US-10-979-159-303
21	398	42.2	111	5	US-10-611-655-4
22	376.5	39.9	158	4	US-10-322-281-17
23	370.5	39.2	114	4	US-10-410-842A-4
24	233.5	24.7	631	4	US-10-433-108-14
25	224.5	23.8	294	4	US-10-433-108-26
26	220	23.3	640	4	US-10-433-108-15
27	214	22.7	284	4	US-10-433-108-24

28	211.5	22.4	287	4	US-10-433-108-23	Sequence 23, Appl
29	210.5	22.3	302	4	US-10-433-108-25	Sequence 25, Appl
30	206.5	21.9	287	4	US-10-433-108-28	Sequence 28, Appl
31	203	21.5	51	5	US-10-450-763-49895	Sequence 49895, A
32	182	19.3	86	5	US-10-997-700-84	Sequence 84, Appl
33	177	18.8	272	4	US-10-433-108-22	Sequence 22, Appl
34	173	18.3	616	4	US-10-433-108-13	Sequence 13, Appl
35	167	17.7	290	3	US-09-969-748C-2	Sequence 2, Appl
36	167	17.7	290	3	US-09-949-039-2	Sequence 2, Appl
37	167	17.7	290	5	US-10-470-987-42	Sequence 42, Appl
38	165.5	17.5	639	5	US-10-775-180-131	Sequence 131, App
39	165.5	17.5	639	5	US-10-775-204-417	Sequence 417, App
40	165.5	17.5	662	5	US-10-775-180-611	Sequence 611, App
41	165.5	17.5	662	5	US-10-775-204-1623	Sequence 1623, Ap
42	165.5	17.5	663	5	US-10-775-180-600	Sequence 600, App
43	165.5	17.5	663	5	US-10-775-204-1609	Sequence 1609, Ap
44	165.5	17.5	664	5	US-10-775-180-598	Sequence 598, App
45	165.5	17.5	664	5	US-10-775-204-1607	Sequence 1607, App

ALIGNMENTS

RESULT 1  
US-10-611-655-10  
; Sequence 10, Application US/10611655  
; Publication No. US20040266993A1  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Glen A.  
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides  
; FILE REFERENCE: 66663-026  
; CURRENT APPLICATION NUMBER: US/10/611,655  
; CURRENT FILING DATE: 2003-06-30  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimeric ThyOx carrier polypeptide containing  
; OTHER INFORMATION: glucagon-like peptide 1  
US-10-611-655-10

Query Match	100.0%;	Score	944;	DB	5;	Length	176;
Best Local Similarity	100.0%;	Pred. No.	7.2e-70;				
Matches	176;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
Qy	1	MHGE	GFTSDVSSYLEGQA	KFI	AWLVKRG	GGGGGGGGGGGGG	SKVTSITACLV
Db	1	MHGE	GFTSDVSSYLEGQA	KFI	AWLVKRG	GGGGGGGGGGGGG	SKVTSITACLV
Qy	61	QSLR	LDCHENTSSSPQI	YFSLTR	ETKXHLV	FGTVG	VEHTYRSRNTFTSKYHMKVLYL
Db	61	QSLR	LDCHENTSSSPQI	YFSLTR	ETKXHLV	FGTVG	VEHTYRSRNTFTSKYHMKVLYL
Qy	121	SAFT	SXDEGTYTTCALH	SGHSP	PISSQNV	TVLRD	KLVCESILLAQNTSHHHHH
Db	121	SAFT	SXDEGTYTTCALH	SGHSP	PISSQNV	TVLRD	KLVCESILLAQNTSHHHHH

RESULT 2  
US-10-611-655-6  
; Sequence 6, Application US/10611655  
; Publication No. US20040266993A1  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Glen A.  
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides  
; FILE REFERENCE: 66663-026  
; CURRENT APPLICATION NUMBER: US/10/611,655  
; CURRENT FILING DATE: 2003-06-30  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0

```
; SEQ ID NO 6
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric ThyOx carrier polypeptide containing
; OTHER INFORMATION: erythropoietin
US-10-611-655-6

Query Match      83.4%; Score 787; DB 5; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 RGGGGGGGGGFFGGGSKVTSLTACLVDQSLRLDCRHNENTSSSPIQYEFSLTRTKKH 90
Db 189 RGGGGGGGGGFFGGGSKVTSLTACLVDQSLRLDCRHNENTSSSPIQYEFSLTRTKKH 248

QY 91 VLFGTGVPETHYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNT 150
Db 249 VLFGTGVPETHYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNT 308

QY 151 VLRLDKLVKCEGISLLAQTSHHHHH 176
Db 309 VLRLDKLVKCEGISLLAQTSHHHHH 334

RESULT 3
US-10-611-655-8
; Sequence 8, Application US/10611655
; Publication No. US2004026693A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides
; FILE REFERENCE: 66663-026
; CURRENT APPLICATION NUMBER: US/10/611,655
; CURRENT FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SuperEpo
US-10-611-655-8

Query Match      83.4%; Score 787; DB 5; Length 334;
Best Local Similarity 100.0%; Pred. No. 1.2e-56;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 RGGGGGGGGGFFGGGSKVTSLTACLVDQSLRLDCRHNENTSSSPIQYEFSLTRTKKH 90
Db 189 RGGGGGGGGGFFGGGSKVTSLTACLVDQSLRLDCRHNENTSSSPIQYEFSLTRTKKH 248

QY 91 VLFGTGVPETHYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNT 150
Db 249 VLFGTGVPETHYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNT 308

QY 151 VLRLDKLVKCEGISLLAQTSHHHHH 176
Db 309 VLRLDKLVKCEGISLLAQTSHHHHH 334

RESULT 4
US-09-918-725-220
; Sequence 220, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
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; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 220
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-220

Query Match      67.5%; Score 637; DB 3; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDQSLRLDCRHNENTSSSPIQYEFSLTRTKKHVLFGTVGVPEHYRSRTN 108
Db 20 QKVTSLTACLVDQSLRLDCRHNENTSSSPIQYEFSLTRTKKHVLFGTVGVPEHYRSRTN 79

QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNTVLRLDKLVKCEGISLLAQN 168
Db 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNTVLRLDKLVKCEGISLLAQN 139

QY 169 TS 170
Db 140 TS 141

RESULT 5
US-10-474-794-220
; Sequence 220, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-220

Query Match      67.5%; Score 637; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.2e-44;
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDQSLRLDCRHNENTSSSPIQYEFSLTRTKKHVLFGTVGVPEHYRSRTN 108
Db 20 QKVTSLTACLVDQSLRLDCRHNENTSSSPIQYEFSLTRTKKHVLFGTVGVPEHYRSRTN 79

QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNTVLRLDKLVKCEGISLLAQN 168
Db 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNTVLRLDKLVKCEGISLLAQN 139

QY 169 TS 170
Db 140 TS 141
```

RESULT 6  
US-10-979-159-220  
; Sequence 220, Application US/10979159  
; Publication No. US20050142138A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/10/979,159  
; CURRENT FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US/09/918,715  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 220  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-979-159-220

Query Match 67.5%; Score 637; DB 5; Length 161;  
Best Local Similarity 100.0%; Pred. No. 1.2e-44;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 49 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 108  
DB 20 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 79  
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168  
DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139  
QY 169 TS 170  
DB 140 TS 141

RESULT 7  
US-10-165-603-32  
; Sequence 32, Application US/10165603  
; Publication No. US20030021792A1  
; GENERAL INFORMATION:  
; APPLICANT: Roben, Paul W  
; APPLICANT: Stevens, Anthony C.  
; TITLE OF INVENTION: TISSUE-SPECIFIC ENDOTHELIAL MEMBRANE  
; TITLE OF INVENTION: PROTEINS  
; FILE REFERENCE: TPTECH.001A  
; CURRENT APPLICATION NUMBER: US/10/165,603  
; CURRENT FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: 60/297,021  
; PRIOR FILING DATE: 2001-06-08  
; PRIOR APPLICATION NUMBER: 60/305,117  
; PRIOR FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-165-603-32

Query Match 66.7%; Score 630; DB 4; Length 161;  
Best Local Similarity 99.2%; Pred. No. 4.5e-44;

Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 49 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 108  
DB 20 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 79  
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168  
DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139  
QY 169 TS 170  
DB 140 TS 141

RESULT 8  
US-10-794-899-66  
; Sequence 66, Application US/10794899  
; Publication No. US20040146516A1  
; GENERAL INFORMATION:  
; APPLICANT: Utah Ventures  
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery  
; FILE REFERENCE: 27110-715  
; CURRENT APPLICATION NUMBER: US/10/794,899  
; CURRENT FILING DATE: 2004-03-05  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 66  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-794-899-66

Query Match 66.7%; Score 630; DB 4; Length 161;  
Best Local Similarity 99.2%; Pred. No. 4.5e-44;  
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 49 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 108  
DB 20 QKVTSLTACLVDSQSLRDCRHEHTSSPIQYFSLTRETCKHVLFGTVGVPHTYRSRTN 79  
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168  
DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139  
QY 169 TS 170  
DB 140 TS 141

RESULT 9  
US-10-287-436A-449  
; Sequence 449, Application US/10287436A  
; Publication No. US20050202421A1  
; GENERAL INFORMATION:  
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER  
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF  
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS  
; FILE REFERENCE: 10872.514696  
; CURRENT APPLICATION NUMBER: US/10/287,436A  
; CURRENT FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: US 60/336,220  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 1446  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 449  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-287-436A-449

Query Match 66.7%; Score 630; DB 5; Length 161;  
Best Local Similarity 99.2%; Pred. No. 4.5e-44;



; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-611-655-1

Query Match 65.4%; Score 617.5; DB 5; Length 162;  
Best Local Similarity 98.4%; Pred. No. 4.8e-43;  
Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 49 QKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKKHLFGTVGVPEHTYRSRTN 108  
Db 20 QKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKKHLFGTVGVPEHTYRSRTN 79  
QY 109 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGHSPPI--SSQNVTVLRLDKLVKCEGISLLAQ 167  
Db 80 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCEGISLLAQ 139  
QY 168 NTS 170  
Db 140 NTS 142

## RESULT 14

US-10-322-281-20  
; Sequence 20, Application US/10322281  
; Publication No. US20040126762A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc S. Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001000  
; CURRENT APPLICATION NUMBER: US/10/322,281  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 159  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-322-281-20

Query Match 63.6%; Score 600; DB 4; Length 159;  
Best Local Similarity 96.7%; Pred. No. 1.3e-41;  
Matches 118; Conservative 1; Mismatches 1; Indels 2; Gaps 1;  
QY 49 QKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKKHLFGTVGVPEHTYRSRTN 108  
Db 20 QKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKKHLFGTVGVPEH--YSRTN 77  
QY 109 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCEGISLLAQ 168  
Db 78 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCEGISLLAQ 137  
QY 169 TS 170  
Db 138 TS 139

## RESULT 15

US-10-450-763-49897  
; Sequence 49897, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 49897  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..(171)  
; OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
US-10-450-763-49897

Query Match 44.9%; Score 424; DB 5; Length 171;  
Best Local Similarity 71.9%; Pred. No. 4.2e-27;  
Matches 92; Conservative 9; Mismatches 21; Indels 6; Gaps 4;  
QY 49 QKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKKHLFGTVGVPEHTYRSRTN 108  
Db 24 QKVTSLTACLVDSLRDCHRENTSSPSKIBFSLTRETCKKHLFGTVGVPEHTYRSRTN 83  
QY 109 FTSKYNMK--VLYLSAFTSKDEGTYTCALHH--SGHSPPI--SSQNVTVL--RDKLVKCEGI 162  
Db 84 FTSKYNMEGPLYTSAPHXARTGTLOVLQPHQFGALSPPIFLSRNVTVVQRTNWKCEGI 143  
QY 163 SLLAQN 170  
Db 144 SLLAQN 151

Search completed: December 6, 2005, 10:47:48  
Job time : 138.979 secs

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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:37:02 ; Search time 7.35888 Seconds  
(without alignments)  
114.521 Million cell updates/sec

Title: US-10-611-655-10

Perfect score: 944

Sequence: 1 MHGEGTFTSDVSSYLEGQAA.....VKCEGISLAQNTSHHHHH 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pap.\*
- 2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pap.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pap.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pap.\*
- 6: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pap.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pap.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	160	16.9	70	US-10-997-061-28	Sequence 28, Appl
2	157	16.6	31	US-10-997-061-3	Sequence 3, Appl
3	156	16.5	277	US-10-997-061-11	Sequence 11, Appl
4	155	16.4	117	US-10-997-061-9	Sequence 9, Appl
5	155	16.4	122	US-10-997-061-31	Sequence 31, Appl
6	154	16.3	31	US-10-997-061-7	Sequence 7, Appl
7	152	16.1	119	US-10-997-061-13	Sequence 13, Appl
8	151	16.0	30	US-10-997-061-1	Sequence 1, Appl
9	151	16.0	31	US-10-997-061-4	Sequence 4, Appl
10	151	16.0	34	US-10-997-061-10	Sequence 10, Appl
11	151	16.0	34	US-10-997-061-12	Sequence 12, Appl
12	148	15.7	30	US-10-997-061-5	Sequence 5, Appl
13	148	15.7	31	US-10-997-061-8	Sequence 8, Appl
14	146	15.5	30	US-10-997-061-2	Sequence 2, Appl
15	144	15.3	259	US-11-054-515-1485	Sequence 1485, Ap
16	143	15.1	30	US-10-997-061-6	Sequence 6, Appl
17	138.5	14.7	256	US-11-054-515-1230	Sequence 1230, Ap
18	135	14.3	259	US-11-054-515-1552	Sequence 1552, Ap
19	134.5	14.2	249	US-11-054-515-1138	Sequence 1138, Ap
20	134	14.2	543	US-10-495-664-3	Sequence 3, Appl
21	131.5	13.9	252	US-11-054-515-1541	Sequence 1541, Ap
22	130.5	13.8	248	US-11-054-515-1254	Sequence 1254, Ap
23	130.5	13.8	618	US-10-512-184-48	Sequence 48, Appl
24	129.5	13.7	249	US-11-054-515-1856	Sequence 1856, Ap
25	129.5	13.7	252	US-11-054-515-1954	Sequence 1954, Ap

ALIGNMENTS

RESULT 1

US-10-997-061-28

; Sequence 28, Application US/10997061

; Publication No. US20050260701A1

; GENERAL INFORMATION:

; APPLICANT: Wagner, Fred W.

; APPLICANT: Luan, Peng

; APPLICANT: Xia, Yuannan

; APPLICANT: Boscard, Mary

; APPLICANT: Holmquist, Barton H.

; APPLICANT: Merrifield, Edwin H.

; APPLICANT: Stridom, Daniel

; APPLICANT: Restoragen Inc.

; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1 (7-36) Amide Peptides

; FILE REFERENCE: 1627.003US1

; CURRENT APPLICATION NUMBER: US/10/997,061

; CURRENT FILING DATE: 2004-11-24

; PRIOR APPLICATION NUMBER: PCT/US03/16469

; PRIOR FILING DATE: 2003-05-23

; PRIOR APPLICATION NUMBER: US 60/383,214

; PRIOR FILING DATE: 2002-05-24

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 70

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: A synthetic peptide

US-10-997-061-28

Query Match 16.9%; Score 160; DB 6; Length 70;

Best Local Similarity 82.1%; Pred. No. 1.3e-08;

Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 HGEFTTSDVSSYLEGQAAKEFTIAWLKRGSGGGGGG 40

Db 4 HAEFTTSDVSSYLEGQAAKEFTIAWLKRGSGGGGGG 42

RESULT 2

US-10-997-061-3

; Sequence 3, Application US/10997061

; Publication No. US20050260701A1

; GENERAL INFORMATION:

; APPLICANT: Wagner, Fred W.

; APPLICANT: Luan, Peng

; APPLICANT: Xia, Yuannan

```

; APPLICANT: Bossard, Mary
; APPLICANT: Holmquist, Barton
; APPLICANT: Merrifield, Edwin H.
; APPLICANT: Strydom, Daniel
; APPLICANT: Restoragen Inc.
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
; FILE REFERENCE: 1627.003US1
; CURRENT APPLICATION NUMBER: US/10/997,061
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16469
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,214
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
;
US-10-997-061-3

Query Match          16.6%; Score 157; DB 6; Length 31;
Best Local Similarity 96.8%; Pred. No. 1e-08;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HGEFTTSDVSSYLEGQAQKEFIAMLVKGRG 32
   |||||
Db 1 HAEGTFTSDVSSYLEGQAQKEFIAMLVKGRG 31

RESULT 3
US-10-997-061-11
; Sequence 11, Application US/10997061
; Publication No. US20050260701A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Luan, Peng
; APPLICANT: Xia, Yuannan
; APPLICANT: Bossard, Mary
; APPLICANT: Holmquist, Barton
; APPLICANT: Merrifield, Edwin H.
; APPLICANT: Strydom, Daniel
; APPLICANT: Restoragen Inc.
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
; FILE REFERENCE: 1627.003US1
; CURRENT APPLICATION NUMBER: US/10/997,061
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16469
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,214
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
;
; NAME/KEY: SITE
; LOCATION: 1
; OTHER INFORMATION: Xaa = T7 tag
;
US-10-997-061-11

Query Match          16.5%; Score 156; DB 6; Length 277;
Best Local Similarity 96.8%; Pred. No. 1.3e-07;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHGEFTTSDVSSYLEGQAQKEFIAMLVKGR 31
   |||||

```

```

Db 2 MHAEFTTSDVSSYLEGQAQKEFIAMLVKGR 32

RESULT 4
US-10-997-061-9
; Sequence 9, Application US/10997061
; Publication No. US20050260701A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Luan, Peng
; APPLICANT: Xia, Yuannan
; APPLICANT: Bossard, Mary
; APPLICANT: Holmquist, Barton
; APPLICANT: Merrifield, Edwin H.
; APPLICANT: Strydom, Daniel
; APPLICANT: Restoragen Inc.
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
; FILE REFERENCE: 1627.003US1
; CURRENT APPLICATION NUMBER: US/10/997,061
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16469
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,214
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
;
; NAME/KEY: SITE
; LOCATION: 1
; OTHER INFORMATION: Xaa = T7-tag
;
US-10-997-061-9

Query Match          16.4%; Score 155; DB 6; Length 117;
Best Local Similarity 75.0%; Pred. No. 6.4e-08;
Matches 33; Conservative 0; Mismatches 9; Indels 2; Gaps 1;

QY 2 HGEFTTSDVSSYLEGQAQKEFIAMLVKGRG--GGGGSGGGGGEF 43
   |||||
Db 9 HAEGTFTSDVSSYLEGQAQKEFIAMLVKGRFLGPDRAEGTF 52

RESULT 5
US-10-997-061-31
; Sequence 31, Application US/10997061
; Publication No. US20050260701A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Luan, Peng
; APPLICANT: Xia, Yuannan
; APPLICANT: Bossard, Mary
; APPLICANT: Holmquist, Barton
; APPLICANT: Merrifield, Edwin H.
; APPLICANT: Strydom, Daniel
; APPLICANT: Restoragen Inc.
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
; FILE REFERENCE: 1627.003US1
; CURRENT APPLICATION NUMBER: US/10/997,061
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16469
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,214
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 122
; TYPE: PRT

```

```

;
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
;
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 14
; OTHER INFORMATION: Xaa = Peptide 5
US-10-997-061-31

```

Query Match	16.4%	Score 155;	DB 6;	Length 122;
Best Local Similarity	75.0%	Pred. No. 6.7e-08;		
Matches 33:	Conservative	0;	Mismatches 9;	Indels 2;
				Gaps 1;

QY 2 HGE~~GT~~TFTSDVSSYLEGQAAKEFIAWLVKGRG--GGGGGGGGGF 43

DB 17 HAEGTFTSDVSSYLEGQAAKEFIAWLVKGRFLGSPDRHAEGTF 60

## RESULT 6

```

US-10-997-061-7
; Sequence 7, Application US/10997061
; Publication No. US20050260701A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Luan, Peng
; APPLICANT: Xia, Yuannan
; APPLICANT: Bossard, Mary
; APPLICANT: Holmquist, Barton
; APPLICANT: Merrifield, Edwin H.
; APPLICANT: Strydom, Daniel
; APPLICANT: Restoragen Inc.
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
; FILE REFERENCE: 1627.003US1
; CURRENT APPLICATION NUMBER: US/10/997,061
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16469
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,214
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 31
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-10-997-061-7

```

Query Match 16.3%; Score 154; DB 6; Length 31;  
Best Local Similarity 93.5%; Pred. No. 1.9e-08;  
Matches 29: Conservative 1; Mismatches 1; Indels 0; Gaps 0;

**Qy** 2 HGEFTTSDVSSYLEGQAKEFIWLVKGRG 32  
| | | | | : | | | | |  
**pb** 1 HAEGFTTSDVSSYLEGQAAREFIWLVKGRG 31

## RESULT 7

US-10-997-061-13  
; Sequence 13, Application US/10997061  
; Publication No. US20050260701A1  
; GENERAL INFORMATION:  
; APPLICANT: Wagner, Fred W.  
; APPLICANT: Luan, Peng  
; APPLICANT: Xia, Yuannan  
; APPLICANT: Bossard, Mary  
; APPLICANT: Holmquist, Barton  
; APPLICANT: Merrifield, Edwin H.  
; APPLICANT: Striydom, Daniel  
; APPLICANT: Restoragen Inc.  
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1 (7-36) Amide Peptides  
; FILE REFERENCE: 1627.003US1

```

; CURRENT APPLICATION NUMBER: US/10/997,061
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16469
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,214
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1
; OTHER INFORMATION: Xaa = T7-tag
; US-10-997-061-13

```

Query Match 16.1%; Score 152; DB 6; Length 119;  
Best Local Similarity 72.7%; Pred. No. 1.2e-07;  
Matches 32; Conservative 1; Mismatches 9; Indels 2; Gaps 1;

## RESULT 8

```

US-10-997-061-1
; Sequence 1, Application US/10997061
; Publication No. US20050260701A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Luan, Peng
; APPLICANT: Xia, Yuannan
; APPLICANT: Bossard, Mary
; APPLICANT: Holmquist, Barton
; APPLICANT: Merrifield, Edwin H.
; APPLICANT: Strydom, Daniel
; APPLICANT: Restoragen Inc.
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1 (7-36) Amide Peptides
; FILE REFERENCE: 1627.003US1
; CURRENT APPLICATION NUMBER: US/10/997,061
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16469
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,214
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-10-997-061-1

```

Query Match 16.0%; Score 151; DB 6; Length 30;  
Best Local Similarity 96.7%; Pred. No. 3.3e-08;  
Matches 29; Conservative 1; Indels 0; Mismatches 0;

Qy 2 HGGTFTSDVSSYLEGQAAKEFIAWLVKGR 31  
| | | | | | | | | | | | | | | | | | | | | |  
nb 1 HAEGTFTSDVSSYLEGQAAKEFIAWLVKGR 30  
| | | | | | | | | | | | | | | | | | | | | |

RESULT 9

US-10-997-061-4  
; Sequence 4, Application US/10997061  
; Publication No. US20050260701A1

```

US-10-997-061-10
Query Match          16.0%; Score 151; DB 6; Length 34;
Best Local Similarity 96.7%; Pred. No. 3.8e-08;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 HGGTFTSDVSSYLEGQAQAEFTIAWLVKGR 31
    | | | | | | | | | | | | | | | | | |
DB  1 HAEGTFTSDVSSYLEGQAQAEFTIAWLVKGR 30

RESULT 11
US-10-997-061-12
; Sequence 12, Application US/10997061
; Publication No. US20050260701A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Luan, Peng
; APPLICANT: Xia, Yuannan
; APPLICANT: Bossard, Mary
; APPLICANT: Holmquist, Barton
; APPLICANT: Merrifield, Edwin H.
; APPLICANT: Strydom, Daniel
; APPLICANT: Restoragen Inc.
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
; FILE REFERENCE: 1627.003US1
; CURRENT APPLICATION NUMBER: US/10/997,061
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16469
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,214
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
; NAME/KEY: SITE
; LOCATION: 34
; OTHER INFORMATION: Xaa = Hse-lactone
US-10-997-061-12

Query Match          16.0%; Score 151; DB 6; Length 34;
Best Local Similarity 96.7%; Pred. No. 3.8e-08;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 HGGTFTSDVSSYLEGQAQAEFTIAWLVKGR 31
    | | | | | | | | | | | | | | | | | |
DB  1 HAEGTFTSDVSSYLEGQAQAEFTIAWLVKGR 30

RESULT 12
US-10-997-061-5
; Sequence 5, Application US/10997061
; Publication No. US20050260701A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, Fred W.
; APPLICANT: Luan, Peng
; APPLICANT: Xia, Yuannan
; APPLICANT: Bossard, Mary
; APPLICANT: Holmquist, Barton
; APPLICANT: Merrifield, Edwin H.
; APPLICANT: Strydom, Daniel
; APPLICANT: Restoragen Inc.
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
; FILE REFERENCE: 1627.003US1
; CURRENT APPLICATION NUMBER: US/10/997,061
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16469

```

```

; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,214
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
US-10-997-061-5

```

```
Query Match      15.7%; Score 148; DB 6; Length 30;
Best Local Similarity 93.3%; Pred. No. 6.1e-08;
Matches 28; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

RESULT 13  
US-10-997-061-8  
; Sequence 8, Application US/10997061  
; Publication No. US20050260701A1  
; GENERAL INFORMATION:  
; APPLICANT: Wagner, Fred W.  
; APPLICANT: Luan, Peng  
; APPLICANT: Xia, Yuannan  
; APPLICANT: Bossard, Mary  
; APPLICANT: Holmquist, Barton  
; APPLICANT: Merrifield, Edwin H.  
; APPLICANT: Strydom, Daniel  
; APPLICANT: Restoragen Inc.  
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides  
; FILE REFERENCE: 1627.003US1  
; CURRENT APPLICATION NUMBER: US/10/997,061  
; CURRENT FILING DATE: 2004-11-24  
; PRIOR APPLICATION NUMBER: PCT/US03/16469  
; PRIOR FILING DATE: 2003-05-23  
; PRIOR APPLICATION NUMBER: US 60/383,214  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 31  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A synthetic peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: 31  
; OTHER INFORMATION: Xaa = Gly-NH2  
US-10-997-061-8

RESULT 14  
US-10-997-061-2  
; Sequence 2, Application US/10997061  
; Publication No. US20050260701A1  
; GENERAL INFORMATION:  
; APPLICANT: Wagner, Fred W.  
; APPLICANT: Luan, Peng

```

; APPLICANT: Xia, Yuannan
; APPLICANT: Bossard, Mary
; APPLICANT: Holmquist, Barton
; APPLICANT: Merrifield, Edwin H.
; APPLICANT: Strydom, Daniel
; APPLICANT: Restoragen Inc.
; TITLE OF INVENTION: Method for Enzymatic Production of GLP-1(7-36) Amide Peptides
; FILE REFERENCE: 1627.003US1
; CURRENT APPLICATION NUMBER: US/10/997,061
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: PCT/US03/16469
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/383,214
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A synthetic peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 30
; OTHER INFORMATION: Xaa = Arg-NH2
US-10-997-061-2

```

Query Match	15.5%	Score 146;	DB 6;	Length 30;
Best Local Similarity	96.8%	Pred. No. 9.2e-08;		
Matches	28;	Conservative 0;	Mismatches 1;	Indels 0; Gaps 0;
Qy	2	HGEGTTSDVSSYLEGQAAKEFTIAWLKVG	30	
Db	1	HAEGTTSDVSSYLEGQAAKEFTIAWLKVG	29	

RESULT 15  
US-11-054-515-1485  
; Sequence 1485, Application US/11054515  
; Publication No. US20050255532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523P3  
; CURRENT APPLICATION NUMBER: US/11/054,515  
; CURRENT FILING DATE: 2005-02-10  
; PRIOR APPLICATION NUMBER: 60/543,296  
; PRIOR FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 60/580,347  
; PRIOR FILING DATE: 2004-06-18  
; PRIOR APPLICATION NUMBER: 10/293,418  
; PRIOR FILING DATE: 2002-11-14  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; Remaining Prior Application data removed - See File Wrapper or P  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 1485  
; LENGTH: 259  
; TYPE: PRT  
; ORGANISM: Homo sapiens



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:12 ; Search time 164.348 Seconds  
(without alignments)  
470.529 Million cell updates/sec

Title: US-10-611-655-10

Perfect score: 944

Sequence: 1 MHGCTFTSDVSSYLEGQAA.....VKCEGISLAQNTSHHHHH 176

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1980s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	944	100.0	176	9	Adw10192 Chimeric
2	787	83.4	334	9	Adw10190 Erythropo
3	787	83.4	334	9	Adw10188 Chimeric
4	637	67.5	161	5	Abb90744 Human Tum
5	637	67.5	161	6	Abu54451 Human Tum
6	630	66.7	161	7	Adp65208 Human Thy
7	630	66.7	161	8	Abu84755 Human can
8	630	66.7	161	9	Adz13572 Human can
9	630	66.7	161	9	Adz13574 Human can
10	630	66.7	161	9	Adz13570 Human can
11	630	66.7	165	3	Aab43939 Human can
12	630	66.7	165	4	Aag73850 Human col
13	617.5	65.4	162	9	Adw10183 Human Thy
14	604	64.0	368	2	Aay31789 Human Thy
15	600	63.6	119	2	Aay31787 Human Thy
16	546	57.8	150	8	Adk98542 Human imm
17	424	44.9	171	4	Abg19538 Novel hum
18	421	44.6	161	2	Aaw53480 Rat Thy-1
19	406.5	43.1	162	5	Abb90786 Mouse Tum
20	406.5	43.1	162	6	Abu54493 Mouse tum
21	406.5	43.1	162	8	Abu84754 Murine ca
22	406.5	43.1	162	8	Adz13567 Murine ca
23	398	42.2	111	9	Adw10186 Thy-1 bas
24	389	41.2	368	2	Aay31788 Rat Thy-1

25	387	41.0	105	3	AAG00166	Aag00166 Human sec
26	385	40.8	119	2	AAY31786	Aay31786 Rat Thy-1
27	370.5	39.2	114	7	ADF12417	Adf12417 Mouse Thy
28	370.5	39.2	114	8	ADG39435	Adg39435 Mouse Thy
29	233.5	24.7	631	6	Aae30917	Aae30917 Val8-GLP-
30	224.5	23.8	71	9	ADM44109	Adm44109 Glucagon-
31	224.5	23.8	294	6	Aae30929	Aae30929 Gly8-Glu2
32	220	23.3	640	6	Aae30918	Aae30918 Gly8-Glu2
33	214	22.7	284	6	Aae30927	Aae30927 Gly8-Glu2
34	211.5	22.4	287	6	Aae30926	Aae30926 Gly8-Glu2
35	210.5	22.3	302	6	Aae30928	Aae30928 Gly8-Glu2
36	206.5	21.9	287	6	Aae30931	Aae30931 Gly8-Glu2
37	203	21.5	51	4	ABG19536	Abg19536 Novel hum
38	182	19.3	86	8	ADJ65908	Adj65908 Inclusion
39	177	18.8	272	6	Aae30925	Aae30925 Gly8-Glu2
40	173	18.3	616	6	Aae30916	Aae30916 Val8-GLP-
41	168	17.8	649	9	ADM45209	Adm45209 K. lactis
42	167	17.7	290	6	ABP55318	Abp55318 Pelb/5AF/
43	167	17.7	290	7	ADL99518	Adl99518 Single ch
44	167	17.7	291	5	Aae29202	Aae29202 Single ch
45	166.5	17.6	646	9	ADM45219	Adm45219 K. lactis

ALIGNMENTS

RESULT 1

ADW10192

ID ADW10192 standard; protein; 176 AA.

XX ADW10192;

DT 24-MAR-2005 (first entry)

XX Chimeric ThyOx carrier containing glucagon-like peptide 1.

DE non-immunoglobulin binding polypeptide; selective binding; ThyOx;

KW glucagon-like peptide 1; GLP-1.

XX Chimeric.

OS Synthetic.

XX US2004266993-A1.

PN 30-DEC-2004.

XX 30-JUN-2003; 2003US-00611655.

XX 30-JUN-2003; 2003US-00611655.

XX (EVAN/) EVANS G A.

PI Evans GA;

XX WPI; 2005-047648/05.

DR N-PSDB; ADM10191.

PT New chimeric non-immunoglobulin binding polypeptide comprises immunoglobulin-like domain containing scaffold and exhibits selective binding activity, for producing non-immunoglobulin binding polypeptides with selective binding activity.

PS Disclosure; SEQ ID NO 10; 45pp; English.

XX The invention relates to a novel chimeric non-immunoglobulin binding polypeptide. The polypeptide comprises an immunoglobulin-like domain containing scaffold with two or more solvent exposed loops containing a different complementarity-determining region (CDR) from a parent antibody inserted into each of the loops and exhibiting selective binding activity toward a ligand bound by the parent antibody. The invention further comprises: a chimeric ThyOx binding polypeptide, comprising one or more altered immunoglobulin-like domain loop regions of a ThyOx family polypeptide or at least one immunoglobulin-like domain containing

CC scaffold derived from a ThyOx family polypeptide, and a heterologous  
 CC binding polypeptide exhibiting selective binding activity toward a non-  
 CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx  
 CC binding polypeptide above. The chimeric non-immunoglobulin binding  
 CC polypeptide is useful for producing non-immunoglobulin binding  
 CC polypeptides having selective binding activity toward a predetermined  
 CC molecule. This sequence represents a chimeric ThyOx carrier containing  
 CC glucagon-like peptide 1 of the invention.  
 XX  
 SQ Sequence 176 AA;

Query Match 100.0%; Score 944; DB 9; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 9.6e-85;  
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHCEGFTSDVSSYLEGQAKEFIAMLVKRGSGGGSGGGGFGGGGSKVTSLSACLVD 60  
 DB 1 MHGEGFTSDVSSYLEGQAKEFIAMLVKRGSGGGSGGGGFGGGGSKVTSLSACLVD 60  
 QY 61 QSLRLDCRHEHTSSSPIQEFSLTRETKKHVLFGTVGPEHTYRSRTNFTSKYHMKVLYL 120  
 DB 61 QSLRLDCRHEHTSSSPIQEFSLTRETKKHVLFGTVGPEHTYRSRTNFTSKYHMKVLYL 120  
 QY 121 SAFTSKDEGTYTCALHSHGSPPISSQNTVLRDLKLVKCEGISLLAQTSHHHHH 176  
 DB 121 SAFTSKDEGTYTCALHSHGSPPISSQNTVLRDLKLVKCEGISLLAQTSHHHHH 176

RESULT 2  
 ADW10190  
 ID ADW10190 standard; protein; 334 AA.  
 AC ADW10190;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Erythropoietin protein, named SuperEpo.  
 XX  
 KW non-immunoglobulin binding polypeptide; selective binding; ThyOx;  
 KW erythropoietin; SuperEpo.

Chimeric.  
 OS Synthetic.  
 OS US2004266993-A1.  
 XX  
 PN 30-DEC-2004.  
 XX  
 PD 30-JUN-2003; 2003US-00611655.  
 XX  
 PF 30-JUN-2003; 2003US-00611655.  
 XX  
 PR 30-JUN-2003; 2003US-00611655.  
 XX  
 PA (EVAN/) EVANS G A.  
 XX  
 PI Evans GA;  
 XX  
 DR WPI; 2005-047648/05.  
 DR N-PSDB; ADW10189.

XX New chimeric non-immunoglobulin binding polypeptide comprises  
 PT immunoglobulin-like domain containing scaffold and exhibits selective  
 PT binding activity, for producing non-immunoglobulin binding polypeptides  
 PT with selective binding activity.  
 XX  
 PS Disclosure; SEQ ID NO 8; 45pp; English.

CC The invention relates to a novel chimeric non-immunoglobulin binding  
 CC polypeptide. The polypeptide comprises an immunoglobulin-like domain  
 CC containing scaffold with two or more solvent exposed loops containing a  
 CC different complementarity-determining region (CDR) from a parent antibody  
 CC inserted into each of the loops and exhibiting selective binding activity  
 CC toward a ligand bound by the parent antibody. The invention further  
 CC comprises a chimeric ThyOx binding polypeptide, comprising one or more

CC altered immunoglobulin-like domain loop regions of a ThyOx family  
 CC polypeptide or at least one immunoglobulin-like domain containing  
 CC scaffold derived from a ThyOx family polypeptide, and a heterologous  
 CC binding polypeptide exhibiting selective binding activity toward a non-  
 CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx  
 CC binding polypeptide above. The chimeric non-immunoglobulin binding  
 CC polypeptide is useful for producing non-immunoglobulin binding  
 CC polypeptides having selective binding activity toward a predetermined  
 CC molecule. This sequence represents an erythropoietin protein, named  
 CC SuperEpo, of the invention.  
 XX  
 SQ Sequence 334 AA;

Query Match 83.4%; Score 787; DB 9; Length 334;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-69;  
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 RGGGGGGGGGGGFGGGGSKVTSLSACLVDQSLRLDCRHEHTSSSPIQEFSLTRETKKH 90  
 DB 189 RGGGGGGGGGGGFGGGGSKVTSLSACLVDQSLRLDCRHEHTSSSPIQEFSLTRETKKH 248  
 QY 91 VLFGTGVPPEHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSPPISSQNT 150  
 DB 249 VLFGTGVPPEHTYRSRTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSPPISSQNT 308  
 QY 151 VLRLDKLVKCEGISLLAQTSHHHHH 176  
 DB 309 VLRLDKLVKCEGISLLAQTSHHHHH 334

RESULT 3  
 ADW10188  
 ID ADW10188 standard; protein; 334 AA.  
 AC ADW10188;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Chimeric ThyOx carrier containing erythropoietin.  
 XX  
 KW non-immunoglobulin binding polypeptide; selective binding; ThyOx;  
 KW erythropoietin.

Chimeric.  
 OS Synthetic.  
 OS US2004266993-A1.  
 XX  
 PN 30-DEC-2004.  
 XX  
 PD 30-JUN-2003; 2003US-00611655.  
 XX  
 PF 30-JUN-2003; 2003US-00611655.  
 XX  
 PR 30-JUN-2003; 2003US-00611655.  
 XX  
 PA (EVAN/) EVANS G A.  
 XX  
 PI Evans GA;  
 XX  
 DR WPI; 2005-047648/05.  
 DR N-PSDB; ADW10187.

XX New chimeric non-immunoglobulin binding polypeptide comprises  
 PT immunoglobulin-like domain containing scaffold and exhibits selective  
 PT binding activity, for producing non-immunoglobulin binding polypeptides  
 PT with selective binding activity.

XX Disclosure; SEQ ID NO 6; 45pp; English.

CC The invention relates to a novel chimeric non-immunoglobulin binding  
 CC polypeptide. The polypeptide comprises an immunoglobulin-like domain  
 CC containing scaffold with two or more solvent exposed loops containing a  
 CC different complementarity-determining region (CDR) from a parent antibody  
 CC inserted into each of the loops and exhibiting selective binding activity

toward a ligand bound by the parent antibody. The invention further comprises: a chimeric ThyOx binding polypeptide, comprising one or more altered immunoglobulin-like domain loop regions of a ThyOx family polypeptide or at least one immunoglobulin-like domain containing scaffold derived from a ThyOx family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non-ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx binding polypeptide above. The chimeric non-immunoglobulin binding polypeptide is useful for producing non-immunoglobulin binding polypeptides having selective binding activity toward a predetermined molecule. This sequence represents a chimeric ThyOx carrier containing erythropoietin of the invention.

RESULT 4	
ABB90744	
ID	ABB90744 standard; protein; 161 AA.
XX	AC
XX	ABB90744;
XX	
XX	30-MAY-2002 (first entry)
XX	
XX	Human Tumour Endothelial Marker polypeptide SEQ ID NO 220.
DE	
XX	
XX	Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
KW	normal endothelial marker; pan-endothelial marker; immunostimulant;
KW	antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
KW	polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
KW	psoriasis.
XX	
XX	Homo sapiens.
OS	
XX	WO200210217-A2.
XX	
PD	07-FEB-2002.
XX	
XX	01-AUG-2001; 2001WO-US024031.
XX	
XX	02-AUG-2000; 2000US-0222599P.
PR	
PR	11-AUG-2000; 2000US-0224360P.
PR	
PR	11-APR-2001; 2001US-0282850P.
XX	
XX	(UYJO ) UNIV JOHNS HOPKINS.
PA	
XX	
PI	St Croix B, Kinzler KW, Vogelstein B;
XX	
DR	WPI; 2002-291856/33.
DR	N-PSDB; ABL92098.
XX	
XX	
PT	An isolated molecule comprising an antibody variable region which
PT	specifically binds to an extracellular domain of a tumor endothelial
PT	marker (TEM) protein, useful for inhibiting tumor growth.
XX	
XX	Claim 35; Page 194; 331pp; English.
PS	
XX	

CC	The invention relates to an isolated molecule comprising an antibody
CC	variable region which specifically binds to an extracellular domain of a
CC	tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
CC	ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
CC	proteins have cytostatic, immunostimulant and antiangiogenic activity.
CC	They are useful for inhibiting tumour growth, neoangiogenesis in subjects
CC	bearing a vascularised tumour, polycystic kidney disease, diabetic
CC	retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
CC	genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
CC	are disclosed, as are marker oligonucleotide sequences: tumour
CC	endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
CC	endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
CC	(PEM) ABL91903-ABL91995
XX	
XX	Sequence 161 AA;
XX	
XX	Query Match 67.5%; Score 637; DB 5; Length 161;
XX	Best Local Similarity 100.0%; Pred. No. 1.6e-54;
XX	Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
QY	49 QKVTSLTACLVDSQLRDCRHEMTSSPIQYFSLRTRTKKHVLFGTVGVPEHTYRSRTN 108
DB	
DB	20 QKVTSLTACLVDSQLRDCRHEMTSSPIQYFSLRTRTKKHVLFGTVGVPEHTYRSRTN 79
DB	
QY	109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDLVKCEGISLLAQN 168
DB	
DB	80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDLVKCEGISLLAQN 139
DB	
QY	169 TS 170
DB	
DB	140 TS 141
DB	
XX	
XX	RESULT 5
XX	ABU54451
ID	ABU54451 standard; protein; 161 AA.
XX	
AC	ABU54451;
XX	
XX	12-MAR-2003 (first entry)
XX	
XX	Human tumour endothelial marker TEM 13.
XX	
XX	Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
XX	Tumour endothelial marker; normal endothelial marker; PEM;
KW	pan-endothelial marker; polycystic kidney disease; psoriasis;
KW	diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
KW	neoangiogenesis; immune response; cytostatic; antidiabetic;
KW	ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
XX	
OS	Homo sapiens.
XX	
XX	WO200283874-A2.
PN	
XX	
FD	24-OCT-2002.
XX	
XX	10-APR-2002; 2002WO-US008253.
XX	
XX	11-APR-2001; 2001US-0282850P.
PR	
PR	06-FEB-2002; 2002US-0354262P.
XX	
XX	(UYJO ) UNIV JOHNS HOPKINS.
XX	
XX	Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
PI	
XX	
DR	WPI; 2003-093016/08.
DR	
XX	N-ESDB; ABX72023.
XX	
XX	New purified human transmembrane protein, designated as tumor endothelial
PT	marker (TEM) 3, useful for detecting, diagnosing or treating tumors,
PT	polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
PT	psoriasis.
PT	

PS Disclosure; Page 206-207; 374pp; English.

XX The present invention relates to a novel method for the isolation of

CC endothelial cells (ECs), and the identification of genes expressed in

CC normal and tumour ECs. Tumour endothelial marker (TEM), normal

CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are

CC identified in human ECs. The human EC marker proteins and the

CC polynucleotide sequences encoding them are useful for detecting,

CC diagnosing or treating tumours as well as polycystic kidney disease,

CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also

CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for

CC inducing an immune response to tumour endothelial cells in a patient, or

CC for identifying candidate drugs for treating tumours. The present

CC sequence represents a human TEM or NEM protein of the invention

XX SQ Sequence 161 AA;

Query Match 67.5%; Score 637; DB 6; Length 161;

Best Local Similarity 100.0%; Pred. No. 1.6e-54;

Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDQSLRDCRHNSTSSPIQYEFSLTRETCKHVLFGTVGVPHTYRSRTN 108

DB 20 QKVTSLTACLVDQSLRDCRHNSTSSPIQYEFSLTRETCKHVLFGTVGVPHTYRSRTN 79

QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSONVTVLDRDKLVKCGISLLAQN 168

DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSONVTVLDRDKLVKCGISLLAQN 139

QY 169 TS 170

DB 140 TS 141

RESULT 6

ADP65208

ID ADP65208 standard; protein; 161 AA.

AC ADP65208;

XX 12-AUG-2004 (first entry)

XX Human Thy-1 cell surface antigen, Thy-1 T-cell antigen.

DE autoimmune disease; arthritis; gene expression analysis;

KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;

KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;

KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;

KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;

KW immune; human.

XX Homo sapiens.

XX WO2003072827-A1.

XX 04-SEP-2003.

XX 31-OCT-2002; 2002WO-US035433.

XX 31-OCT-2001; 2001US-0336220P.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Hirsch R, Thorton SL;

XX WPI; 2003-712740/67.

XX GENBANK; NP\_006279.

XX Diagnosing and analyzing autoimmune disease using gene expression

PT profiles and microarray technology, useful for diagnosing and treating

PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and

PT gout.

XX

PS Disclosure; Page; 56pp; English.

XX The invention relates to a novel method for diagnosing and analysing

CC autoimmune disease or arthritides. The method comprises obtaining a

CC patient sample containing mRNA, analysing gene expression using the mRNA

CC that results in a gene expression signature of the mRNA, and using that

CC gene expression signature to diagnose or analyse the autoimmune disease

CC or arthritides in the patient, where gene expression of at least 60% of

CC the genes correlates with that of the gene signature. The invention

CC further comprises: a treatment of rheumatoid arthritis; identification of

CC genes for targeting in the treatment of rheumatoid arthritis in a mammal

CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an

CC array or gene chip, specific for rheumatoid arthritis; diagnosis or

CC analyses of autoimmune disease or rheumatoid arthritis; screening the

CC efficacy of a candidate drug in vitro for the treatment of collagen-

CC induced arthritis; and reducing the symptoms associated with collagen-

CC induced arthritis. The compositions of the invention have the following

CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,

CC antigout, antiinflammatory, dermatological, and immunomodulatory. The

CC methods and compositions of the present invention are useful for

CC diagnosing and treating autoimmune disease or arthritides, such as

CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,

CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an

CC immune disease caused by an infectious agent. This sequence represents a

CC protein sequence relating to the genes used in the analysis and treatment

CC of autoimmune diseases or arthritides. Note: This sequence is not shown

CC in the specification. It has been supplied in an electronic format from

CC WIPO.

XX SQ Sequence 161 AA;

Query Match 66.7%; Score 630; DB 7; Length 161;

Best Local Similarity 99.2%; Pred. No. 7.9e-54;

Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDQSLRDCRHNSTSSPIQYEFSLTRETCKHVLFGTVGVPHTYRSRTN 108

DB 20 QKVTSLTACLVDQSLRDCRHNSTSSPIQYEFSLTRETCKHVLFGTVGVPHTYRSRTN 79

QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSONVTVLDRDKLVKCGISLLAQN 168

DB 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSONVTVLDRDKLVKCGISLLAQN 139

QY 169 TS 170

DB 140 TS 141

RESULT 7

ABO84755

ID ABO84755 standard; protein; 161 AA.

AC ABO84755;

XX 18-NOV-2004 (first entry)

XX Human cancer-associated protein (CAP) HP07-003.

DE Human; cancer-associated protein; CAP; cancer; cytostatic.

KW Homo sapiens.

XX WO2004058146-A2.

XX 15-JUL-2004.

XX 15-DEC-2003; 2003WO-US040081.

XX 17-DEC-2002; 2002US-00322281.

XX (SAGR-) SAGRES DISCOVERY INC.

XX Morris DW, Malandro MS;

XX WPI; 2004-499109/47.  
DR N-PSDB; ABD33081.  
XX  
PT Novel human cancer associated protein encoded within open reading frame  
PT of cancer associated gene, useful as targets for diagnosing cancer.  
XX  
PS Claim 18; SEQ ID NO 20; 182pp; English.  
XX  
XX The invention relates to cancer-associated proteins (CAP) and the cancer-  
XX associated (CA) nucleic acids encoding them. The invention also relates  
XX to a method for treating cancers involving administering to a patient an  
XX inhibitor of CAP, and a method of screening for anticancer activity in a  
XX potential drug involving providing a cell that expresses a CA gene,  
XX contacting a tissue sample derived from a cancer cell with an anticancer  
XX drug candidate and monitoring the effect of the anticancer drug candidate  
XX on expression of the CA gene. The CAP proteins are useful for detecting  
XX cancer associated with expression of a CAP protein in a test cell sample  
XX and for screening for a bioactive agent capable of modulating the  
XX activity of a CAP protein. The CA nucleic acids are useful for diagnosing  
XX cancer, involving determining the expression of a CA nucleic acid in a  
XX tissue. This sequence represents a human CAP of the invention. Note: The  
XX sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 161 AA;  
Query Match 66.7%; Score 630; DB 8; Length 161;  
Best Local Similarity 99.2%; Pred. No. 7.9e-54;  
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 49 QKVTSLTACLVDQSLRDLCDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 108  
DB 20 QKVTSLTACLVDQSLRDLCDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 79  
QY 109 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168  
DB 80 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139  
QY 169 TS 170  
DB 140 TS 141  
RESULT 8  
ADZ13572  
ID ADZ13572 standard; protein; 161 AA.  
XX  
AC ADZ13572;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Human cancer-associated protein #329.  
XX  
XX Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;  
XX cytostatic.  
XX  
OS Homo sapiens.  
XX  
XX WO2005031001-A2.  
XX  
XX 07-APR-2005.  
XX  
XX 23-SEP-2004; 2004WO-US031617.  
XX  
XX 23-SEP-2003; 2003US-00669920.  
XX  
XX (CHIR ) CHIRON CORP.  
XX  
XX Morris DW, Malandro MS;  
XX  
XX WPI; 2005-273395/28.  
DR

DR N-PSDB; ADZ13571.  
XX  
XX Nucleic acid array useful for detecting cancer associated nucleic acid,  
XX comprises two or more nucleic acid probes.  
XX  
XX Disclosure; SEQ ID NO 1092; 198pp; English.  
XX  
XX The invention relates to a nucleic acid array for detecting a cancer  
XX associated (CA) nucleic acid, comprising two or more nucleic acid probes.  
XX The invention also relates to a peptide array comprising two or more  
XX isolated polypeptides encoded by a CA nucleic acid sequence, a compound  
XX that binds to a polypeptide, an isolated antibody or its fragment which  
XX binds to a polypeptide, which is prepared by immunizing a host animal  
XX with a composition comprising the polypeptide or its antigen binding  
XX fragment and collecting cells from the host expressing antibodies against  
XX the antigen or its antigen binding fragment, a composition comprising the  
XX antibody and a carrier, a method of screening for anticancer activity, a  
XX method of detecting a CA nucleic acid, a method of inhibiting expression of a CA  
XX nucleic acid in a cell. The CA nucleic acids are useful for detecting a CA  
XX nucleic acid. The antibody is useful for detecting the presence or  
XX absence of cancer cells in an individual which involves contacting cells  
XX from the individual with the antibody and detecting a complex of a CA  
XX protein from the cancer cells and the antibody, where the detection of  
XX the complex correlates with the presence of cancer cells in the  
XX individual. The composition is useful for inhibiting growth of cancer  
XX cells in an individual or for delivering a therapeutic agent to cancer  
XX cells in an individual. The invention is also useful for diagnosing  
XX cancer, for treating cancer and for inhibiting expression of a CA gene in  
XX a cell. This sequence represents a human cancer-associated protein of the  
XX invention.  
XX  
XX Sequence 161 AA;  
Query Match 66.7%; Score 630; DB 9; Length 161;  
Best Local Similarity 99.2%; Pred. No. 7.9e-54;  
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 49 QKVTSLTACLVDQSLRDLCDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 108  
DB 20 QKVTSLTACLVDQSLRDLCDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 79  
QY 109 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 168  
DB 80 FTSKYNMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGISLLAQN 139  
QY 169 TS 170  
DB 140 TS 141  
RESULT 9  
ADZ13574  
ID ADZ13574 standard; protein; 161 AA.  
XX  
AC ADZ13574;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
XX Human cancer-associated protein #330.  
XX  
XX Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;  
XX cytostatic.  
XX  
OS Homo sapiens.  
XX  
XX WO2005031001-A2.  
XX  
XX 07-APR-2005.  
XX  
XX 23-SEP-2004; 2004WO-US031617.  
XX  
XX 23-SEP-2003; 2003US-00669920.  
XX  
XX

XX PA (CHIR ) CHIRON CORP.  
XX PI Morris DW, Malandro MS;  
XX DR WPI; 2005-273395/28.  
XX DR N-PSDB; ADZ13573.  
XX PT Nucleic acid array useful for detecting cancer associated nucleic acid,  
XX PT comprises two or more nucleic acid probes.  
XX PS Disclosure; SEQ ID NO 1094; 198pp; English.  
XX CC The invention relates to a nucleic acid array for detecting a cancer  
XX CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.  
XX CC The invention also relates to a peptide array comprising two or more  
XX CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound  
XX CC that binds to a polypeptide, an isolated antibody or its fragment which  
XX CC binds to a polypeptide, which is prepared by immunizing a host animal  
XX CC with a composition comprising the polypeptide or its antigen binding  
XX CC fragment and collecting cells from the host expressing antibodies against  
XX CC the antigen or its antigen binding fragment, a composition comprising the  
XX CC antibody and a carrier, a method of screening for anticancer activity, a  
XX CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a  
XX CC method of treating cancer and a method of inhibiting expression of a CA  
XX CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA  
XX CC nucleic acids. The antibody is useful for detecting the presence or  
XX CC absence of cancer cells in an individual which involves contacting cells  
XX CC from the individual with the antibody and detecting a complex of a CA  
XX CC protein from the cancer cells and the antibody, where the detection of  
XX CC the complex correlates with the presence of cancer cells in the  
XX CC individual. The composition is useful for inhibiting growth of cancer  
XX CC cells in an individual or for delivering a therapeutic agent to cancer  
XX CC cells in an individual. The invention is also useful for diagnosing  
XX CC cancer, for treating cancer and for inhibiting expression of a CA gene in  
XX CC a cell. This sequence represents a human cancer-associated protein of the  
XX CC invention.  
XX SQ Sequence 161 AA;  
SQ Query Match 66.7%; Score 630; DB 9; Length 161;  
Best Local Similarity 99.2%; Pred. No. 7.9e-54;  
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 49 QKVTSLTACLVDQSLRDCRHEHTSSSPIOYEFSLTRETKKHVLFGTVGVPEHTYRSRN 108  
Db 20 QKVTSLTACLVDQSLRDCRHEHTSSSPIOYEFSLTRETKKHVLFGTVGVPEHTYRSRN 79  
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDKLVKCEGISLLAQN 168  
Db 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDKLVKCEGISLLAQN 139  
QY 169 TS 170  
Db 140 TS 141  
RESULT 10  
ADZ13570  
ID ADZ13570 standard; protein; 161 AA.  
XX AC ADZ13570;  
XX DT 16-JUN-2005 (first entry)  
XX DE Human cancer-associated protein #328.  
XX KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;  
XX KW cytostatic.  
XX OS Homo sapiens.  
XX PN WO2005031001-A2.

XX PD 07-APR-2005.  
XX PF 23-SEP-2004; 2004WO-US031617.  
XX PR 23-SEP-2003; 2003US-00669920.  
XX PA (CHIR ) CHIRON CORP.  
XX PI Morris DW, Malandro MS;  
XX DR WPI; 2005-273395/28.  
XX DR N-PSDB; ADZ13569.  
XX PT Nucleic acid array useful for detecting cancer associated nucleic acid,  
XX PT comprises two or more nucleic acid probes.  
XX PS Disclosure; SEQ ID NO 1090; 198pp; English.  
XX CC The invention relates to a nucleic acid array for detecting a cancer  
XX CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.  
XX CC The invention also relates to a peptide array comprising two or more  
XX CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound  
XX CC that binds to a polypeptide, an isolated antibody or its fragment which  
XX CC binds to a polypeptide, which is prepared by immunizing a host animal  
XX CC with a composition comprising the polypeptide or its antigen binding  
XX CC fragment and collecting cells from the host expressing antibodies against  
XX CC the antigen or its antigen binding fragment, a composition comprising the  
XX CC antibody and a carrier, a method of screening for anticancer activity, a  
XX CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a  
XX CC method of treating cancer and a method of inhibiting expression of a CA  
XX CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA  
XX CC nucleic acids. The antibody is useful for detecting the presence or  
XX CC absence of cancer cells in an individual which involves contacting cells  
XX CC from the individual with the antibody and detecting a complex of a CA  
XX CC protein from the cancer cells and the antibody, where the detection of  
XX CC the complex correlates with the presence of cancer cells in the  
XX CC individual. The composition is useful for inhibiting growth of cancer  
XX CC cells in an individual or for delivering a therapeutic agent to cancer  
XX CC cells in an individual. The invention is also useful for diagnosing  
XX CC cancer, for treating cancer and for inhibiting expression of a CA gene in  
XX CC a cell. This sequence represents a human cancer-associated protein of the  
XX CC invention.  
XX SQ Sequence 161 AA;  
SQ Query Match 66.7%; Score 630; DB 9; Length 161;  
Best Local Similarity 99.2%; Pred. No. 7.9e-54;  
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 49 QKVTSLTACLVDQSLRDCRHEHTSSSPIOYEFSLTRETKKHVLFGTVGVPEHTYRSRN 108  
Db 20 QKVTSLTACLVDQSLRDCRHEHTSSSPIOYEFSLTRETKKHVLFGTVGVPEHTYRSRN 79  
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDKLVKCEGISLLAQN 168  
Db 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNVTVLRDKLVKCEGISLLAQN 139  
QY 169 TS 170  
Db 140 TS 141  
RESULT 11  
AAB43939  
ID AAB43939 standard; protein; 165 AA.  
XX AC AAB43939;  
XX DT 08-FEB-2001 (first entry)  
XX DE Human cancer associated protein sequence SEQ ID NO:1384.  
XX

KW Human; cancer associated gene; cancer antigen; detection; cancer;  
KW diagnosis; cytostatic; proliferative; vulnary; immunomodulator;  
KW antidiabetic; antiaesthetic; antirheumatic; antiarthritic; antiviral;  
KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
KW vasotropic; antiporiatic; antiangiogenic; gene therapy; inflammation;  
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
KW allergic reaction; graft versus host disease; organ rejection;  
KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
KW neurological disease; drug screening.  
XX  
OS Homo sapiens.  
XX  
XX WO200055350-A1.  
PN  
XX  
XX 21-SEP-2000.  
PD  
XX  
XX 08-MAR-2000; 2000WO-US005882.  
PF  
XX  
XX 12-MAR-1999; 99US-0124270P.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM;  
PI  
XX  
XX WPI; 2000-587533/55.  
DR  
XX  
XX N-PSDB; AAC78148.  
DR  
XX  
XX Novel isolated nucleic acids comprising sequences encoding peptides  
PT useful for treating or diagnosing e.g. cancer.  
PT  
XX  
XX Claim 11; Page 2053-2054; 2352pp; English.  
PS  
XX  
XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
CC AAB43398 to AAB44239. The proteins can have activities based on the  
CC tissues and cells the genes are expressed in. Example of activities  
CC include: cytostatic; proliferative; vulnary; immunomodulator;  
CC antidiabetic; antiaesthetic; antirheumatic; antiarthritic;  
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
CC nootropic; vasotropic; antiporiatic and antiangiogenic. The  
CC polynucleotides and polypeptides can be used for preventing, treating or  
CC ameliorating medical conditions and diagnosing pathological conditions.  
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
CC the present invention may be used to treat immune disorders by activating  
CC or inhibiting the proliferation, differentiation or mobilisation of  
CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
CC disorders, allergic reactions, graft versus host disease and organ  
CC rejection, modulate haemostatic or thrombolytic activity, modulate  
CC inflammation, cancers, cardiovascular disorders, neurological disease and  
CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
CC the present invention  
XX  
XX SQ Sequence 165 AA;

Query Match 66.7%; Score 630; DB 3; Length 165;  
Best Local Similarity 99.2%; Pred. No. 8.2e-54;  
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDOSLRDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 108  
DB 24 QKVTSLTACLVDOSLRDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 83  
QY 109 FTSKYRMKVLYLSAFTSKDEGTYTTCALHSHGSHPPISSQNVTVLRDKLVKCEGISLLAQN 168  
DB 84 FTSKYRMKVLYLSAFTSKDEGTYTTCALHSHGSHPPISSQNVTVLRDKLVKCEGISLLAQN 143  
QY 169 TS 170  
DB 144 TS 145

RESULT 12  
AAG73850  
ID AAG73850 standard; protein; 165 AA.  
XX  
AC AAG73850;  
DT 03-SEP-2001 (first entry)  
XX  
XX Human colon cancer antigen protein SEQ ID NO:4614.  
DE  
XX  
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KW colorectal carcinoma; chromosome 11.  
KW  
XX Homo sapiens.  
XX  
XX WO200122920-A2.  
PN  
XX  
XX 05-APR-2001.  
PD  
XX  
XX 28-SEP-2000; 2000WO-US026524.  
PF  
XX  
XX 29-SEP-1999; 99US-0157137P.  
PR  
XX  
XX 03-NOV-1999; 99US-0163280P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ruben SM, Barash SC, Birse CE, Rosen CA;  
PI  
XX  
XX WPI; 2001-235357/24.  
DR  
XX  
XX N-PSDB; AAB33281.  
DR  
XX  
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
PT useful for preventing, diagnosing and/or treating colorectal cancers.  
PT  
XX  
XX Claim 11; Page 6411-6412; 9803pp; English.  
PS  
XX  
XX AAB32943 to AAB37195 and AAG73514 to AAG77788 represent human colon  
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
CC proteins are collectively known as colon cancer antigens. The colon  
CC cancer antigens have cytostatic activity and can be used in gene therapy  
CC and vaccine production. N and P may be used in the prevention, diagnosis  
CC and treatment of diseases associated with inappropriate P expression. For  
CC example, N and P may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of P by expressing inactive proteins or to  
CC supplement the patient's own production of P. Additionally, N may be used  
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids  
CC into a host cell and culturing the cell to express the proteins. N and P  
CC can be used in the prevention, diagnosis and treatment of colorectal  
CC carcinomas and cancers. AAB37196 to AAB37204 and AAB77789 represent  
CC sequences used in the exemplification of the present invention. N.B.  
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
CC to 1052, 7921 and 7922  
XX  
XX SQ Sequence 165 AA;

Query Match 66.7%; Score 630; DB 4; Length 165;  
Best Local Similarity 99.2%; Pred. No. 8.2e-54;  
Matches 121; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 49 QKVTSLTACLVDOSLRDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 108  
DB 24 QKVTSLTACLVDOSLRDCHRENTSSPIQYFSLTRETCKHVLFGTVGVPEHTYRSRTN 83  
QY 109 FTSKYRMKVLYLSAFTSKDEGTYTTCALHSHGSHPPISSQNVTVLRDKLVKCEGISLLAQN 168  
DB 84 FTSKYRMKVLYLSAFTSKDEGTYTTCALHSHGSHPPISSQNVTVLRDKLVKCEGISLLAQN 143  
QY 169 TS 170  
DB 144 TS 145

```
RESULT 13
ADW10183
ID ADW10183 standard; protein; 162 AA.
XX
XX ADW10183;
XX
DT 24-MAR-2005 (first entry)
XX
DE Human Thy-1 protein.
XX
KW non-immunoglobulin binding polypeptide; selective binding; Thy-1.
XX
XX Homo sapiens.
XX
OS US2004266993-A1.
XX
PN 30-DEC-2004.
XX
PD
XX
XX 30-JUN-2003; 2003US-00611655.
XX
PF
XX
XX 30-JUN-2003; 2003US-00611655.
XX
PR
XX
XX (EVAN/) EVANS G A.
XX
PA
XX
PI Evans GA;
XX
XX WPI; 2005-047648/05.
XX
DR
XX
XX New chimeric non-immunoglobulin binding polypeptide comprises
PT immunoglobulin-like domain containing scaffold and exhibits selective
PT binding activity, for producing non-immunoglobulin binding polypeptides
PT with selective binding activity.
XX
XX Disclosure; SEQ ID NO 1; 45pp; English.
XX
PS
XX
XX The invention relates to a novel chimeric non-immunoglobulin binding
CC polypeptide. The polypeptide comprises an immunoglobulin-like domain
CC containing scaffold with two or more solvent exposed loops containing a
CC different complementarity-determining region (CDR) from a parent antibody
CC inserted into each of the loops and exhibiting selective binding activity
CC toward a ligand bound by the parent antibody. The invention further
CC comprises a chimeric ThyOx binding polypeptide, comprising one or more
CC altered immunoglobulin-like domain loop regions of a ThyOx family
CC polypeptide or at least one immunoglobulin-like domain containing
CC scaffold derived from a ThyOx family polypeptide, and a heterologous
CC binding polypeptide exhibiting selective binding activity toward a non-
CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx
CC binding polypeptide above. The chimeric non-immunoglobulin binding
CC polypeptide is useful for producing non-immunoglobulin binding
CC polypeptides having selective binding activity toward a predetermined
CC molecule. This sequence represents a human Thy-1 protein of the
CC invention.
XX
XX Sequence 162 AA;
SQ
Query Match 65.4%; Score 617.5; DB 9; Length 162;
Best Local Similarity 98.4%; Pred. No. 1.4e-52;
Matches 121; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 49 QKVTSLTACLVDQSLDRCRHEHTSSPIQYBESLRTRETKGKVLFGTVGVPHTYRSRTN 108
Db 20 QKVTSLTACLVDQSLDRCRHEHTSSPIQYBESLRTRETKGKVLFGTVGVPHTYRSRTN 79
QY 109 FTSKYMVKVLYLSAFTSKDEGTYTCALHSHSGSPPI-SSQNTVTVLDRDKLVKCEGISLLAQ 167
Db 80 FTSKYMVKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNTVTVLDRDKLVKCEGISLLAQ 139
QY 168 NTS 170
Db 140 NTS 142
```

```
RESULT 14
AAY31789
ID AAY31789 standard; protein; 368 AA.
XX
XX AAY31789;
XX
DT 17-OCT-2003 (revised)
DT 06-DEC-1999 (first entry)
XX
DE Human Thy-1-human IgG constant region fusion protein.
XX
XX Thy-1; human; IgG; angiogenesis; cancer; tumour; rheumatoid arthritis;
KW atherosclerosis; therapy.
XX
XX Homo sapiens.
XX
OS Chimeric.
XX
XX Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Thy-1 signal peptide"
FT Protein 18..368
FT /note= "Thy-1-Ig fusion, specifically claimed in Claim 8"
XX
XX WO9945951-A2.
XX
XX 16-SEP-1999.
XX
XX 11-MAR-1999; 99WO-US005256.
XX
XX 11-MAR-1998; 98US-00077524.
XX
XX (HARD ) HARVARD COLLEGE.
XX (HABE/) HABER C.
XX
XX Haber E, Shaw S, Jain MK, Lee W;
XX
XX WPI; 1999-561618/47.
XX N-PSDB; AAX87980.
XX
XX Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting
PT angiogenesis.
XX
XX Claim 8; Page 46-47; 47pp; English.
XX
XX The present sequence represents a fusion protein, the mature region of
CC which is claimed, comprising the human Thy-1 extracellular region (see
CC AAY31787) and the constant region (hinge, CH2, CH3) of human IgG1. A
CC claimed method for inhibiting angiogenesis in a mammal comprises
CC administering a compound that inhibits Thy-1 associated proliferation of
CC an endothelial cell. The compound is preferably the extracellular region
CC of rat or human Thy-1. The method is used in the treatment of a mammal
CC having a tumour (e.g. by reducing vascularisation), atherosclerosis or
CC rheumatoid arthritis, the lesions of which may be associated with
CC neovascularisation (all claimed). Another claimed method for inhibiting
CC angiogenesis involves administering a Thy-1 antisense nucleic acid or a
CC Thy-1-specific antibody linked to a cytotoxic agent. A method for
CC promoting angiogenesis involves administering a compound that increases
CC Thy-1 expression in an endothelial cell such as a chimeric protein
CC comprising the Thy-1 extracellular fragment and the constant region of an
CC immunoglobulin. (Updated on 17-OCT-2003 to standardise OS field)
XX
XX Sequence 368 AA;
SQ
Query Match 64.0%; Score 604; DB 2; Length 368;
Best Local Similarity 91.3%; Pred. No. 8.2e-51;
Matches 116; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
QY 49 QKVTSLTACLVDQSLDRCRHEHTSSPIQYBESLRTRETKGKVLFGTVGVPHTYRSRTN 108
Db 20 QKVTSLTACLVDQSLDRCRHEHTSSPIQYBESLRTRETKGKVLFGTVGVPHTYRSRTN 79
QY 109 FTSKYMVKVLYLSAFTSKDEGTYTCALHSHSGSPPISSQNTVTVLDRDKLVKCEGISLLAQ 168
```

Db 80 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSHPPISSQNVTVLRDKLVKCEGADLSRP 139  
QY 169 TSHHHH 175  
Db 140 KSSDKTH 146

Search completed: December 6, 2005, 10:36:50  
Job time : 165.348 secs

RESULT 15  
AAY31787  
ID AAY31787 standard; protein; 119 AA.  
XX AC AAY31787;  
XX DT 06-DEC-1999 (first entry)  
XX DE Human Thy-1 extracellular fragment.  
XX KW Thy-1; human; angiogenesis; cancer; tumour; rheumatoid arthritis;  
XX KW atherosclerosis; therapy.  
XX OS Homo sapiens.  
XX PN WO9945951-A2.  
XX PD 16-SEP-1999.  
XX PF 11-MAR-1999; 99WO-US005256.  
XX PR 11-MAR-1998; 98US-00077524.  
XX PA (HARD ) HARVARD COLLEGE.  
XX PA (HABE/) HABER C.  
XX PI Haber E, Shaw S, Jain MK, Lee W;  
XX WPI; 1999-561618/47.  
XX Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting  
XX angiogenesis.  
XX Claim 6; Page 4; 47pp; English.  
XX The present sequence represents the extracellular region of human Thy-1,  
XX a protein expressed by vascular endothelial cells during angiogenesis. A  
XX claimed method for inhibiting angiogenesis in a mammal comprises  
XX administering a compound that inhibits Thy-1 associated proliferation of  
XX an endothelial cell. This compound is preferably the extracellular region  
XX of human or rat (see AAY31786) Thy-1. The method is used in the treatment  
XX of a mammal having a tumour (e.g. by reducing vascularisation),  
XX atherosclerosis and rheumatoid arthritis, the lesions of which may be  
XX associated with neovascularisation (all claimed). Another claimed method  
XX for inhibiting angiogenesis involves administering a Thy-1 antisense  
XX nucleic acid or a Thy1-specific antibody linked to a cytotoxic agent. A  
XX method for promoting angiogenesis involves administering a compound that  
XX increases Thy-1 expression in an endothelial cell such as a chimeric  
XX protein comprising the Thy-1 extracellular fragment and the constant  
XX region of an immunoglobulin (see AAY31788)

Query Match 63.6%; Score 600; DB 2; Length 119;  
Best Local Similarity 98.3%; Pred. No. 4.9e-51;  
Matches 114; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 49 QKVTSLTACLVDSQSLRDCHENTSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 108  
Db 1 QKVTSLTACLVDSQSLRDCHENTSSPIQYEFSLTRETKKHVLFGTVGVPEHTYRSRTN 60  
QY 109 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSHPPISSQNVTVLRDKLVKCEGADLS 164  
Db 61 FTSKYHMKVLYLSAFTSKDEGTYTCALHHSHPPISSQNVTVLRDKLVKCEGADLS 116

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:37:02 ; Search time 4.64111 Seconds  
(without alignments)  
114.521 Million cell updates/sec

Title: US-10-611-655-4

Perfect score: 605

Sequence: 1 QVSRGQKVTSLTACLVDSQL.....VLRDKLVKCEGVYRYFDY 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:\*

- 1: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 2: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 5: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 7: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	118	19.5	121	7	US-11-108-135-28
2	115	19.0	122	6	US-10-932-334-73
3	109	18.0	120	6	US-10-932-334-71
4	109	18.0	120	6	US-10-932-334-72
5	101	16.7	248	6	US-10-512-184-36
6	101	16.7	615	6	US-10-512-184-50
7	100	16.5	121	7	US-11-108-135-24
8	100	16.5	123	6	US-10-932-334-87
9	100	16.5	123	6	US-10-932-334-88
10	100	16.5	123	6	US-10-932-334-92
11	100	16.5	124	6	US-10-932-334-7
12	100	16.5	124	6	US-10-932-334-13
13	100	16.5	124	6	US-10-932-334-70
14	100	16.5	143	6	US-10-932-334-52
15	99	16.4	98	6	US-10-932-334-57
16	97.5	16.1	248	7	US-11-054-515-2088
17	97	16.0	247	7	US-11-054-515-2103
18	96	15.9	120	6	US-10-932-334-74
19	92	15.2	120	7	US-11-173-071-2
20	92	15.2	121	6	US-10-507-662-25
21	92	15.2	121	6	US-10-507-662-26
22	90	14.9	138	7	US-11-089-872-3
23	87	14.4	255	7	US-11-054-515-2087
24	87	14.4	257	7	US-11-054-515-1514
25	86	14.2	115	6	US-10-932-334-80

Sequence 21, Appl  
Sequence 1919, Ap  
Sequence 2084, Ap  
Sequence 1995, Ap  
Sequence 32, Appl  
Sequence 57, Appl  
Sequence 21, Appl  
Sequence 47, Appl  
Sequence 50, Appl  
Sequence 50, Appl  
Sequence 35, Appl  
Sequence 77, Appl  
Sequence 79, Appl  
Sequence 12, Appl  
Sequence 14, Appl  
Sequence 29, Appl  
Sequence 1418, Ap  
Sequence 1672, Ap  
Sequence 30, Appl

26 86 14.2 121 6 US-10-502-145-21  
27 86 14.2 245 7 US-11-054-515-1919  
28 85 14.0 242 7 US-11-054-515-2084  
29 84.5 14.0 248 7 US-11-054-515-1995  
30 84 13.9 118 6 US-10-507-662-32  
31 84 13.9 125 7 US-11-096-074-57  
32 83.5 13.8 247 6 US-11-084-717-21  
33 83 13.7 118 6 US-10-932-334-75  
34 82.5 13.6 114 7 US-11-065-943-47  
35 82 13.6 116 7 US-11-096-074-50  
36 82 13.6 118 6 US-10-507-662-35  
37 82 13.6 120 6 US-10-932-334-77  
38 82 13.6 120 6 US-10-932-334-79  
39 82 13.6 121 6 US-10-932-334-81  
40 82 13.6 128 7 US-11-173-071-12  
41 82 13.6 128 7 US-11-173-071-14  
42 82 13.6 136 6 US-10-839-799-29  
43 82 13.6 253 7 US-11-054-515-1418  
44 82 13.6 253 7 US-11-054-515-1672  
45 81 13.4 118 6 US-10-507-662-30

#### ALIGNMENTS

##### RESULT 1

US-11-108-135-28  
; Sequence 28, Application US/11108135  
; Publication No. US20050260213A1  
; GENERAL INFORMATION:  
; APPLICANT: Koenig, Scott  
; APPLICANT: Veri, Maria Concetta  
; APPLICANT: Tuailon, Nadine  
; APPLICANT: Bonvini, Ezio  
; APPLICANT: Stavenhagen, Jeffrey  
; APPLICANT: Rankin, Christopher  
; TITLE OF INVENTION: FC-gamma-RIIB-specific antibodies and methods of use thereof  
; FILE REFERENCE: 11183-014-999  
; CURRENT APPLICATION NUMBER: US/11/108,135  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/562,804  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 60/582,044  
; PRIOR FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: US 60/582,045  
; PRIOR FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: US 60/654,713  
; PRIOR FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 28  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: mus sp.  
; FEATURE:  
; OTHER INFORMATION: Mouse 2B6 heavy chain variable region  
US-11-108-135-28

Query Match 19.5%; Score 118; DB 7; Length 121;  
Best Local Similarity 33.3%; Pred. No. 9.2e-07;  
Matches 29; Conservative 14; Mismatches 42; Indels 2; Gaps 1;  
QY 1 QVSRGQKVTSLTACLVDSQLRDCRHNTSSNNYWHFSLTRTKKHLVFGTTDPADSYT 60  
Db 1 QVQLQCPVTELVLR--PGASVMTLSCKASDYPFTNYIHWVKRPGQGLEWIGVIDPSDTYP 58  
QY 61 SYNQNFKDEGTYTCALHSHGSHPPISS 87  
Db 59 NYNKKFKGKATLTVVVVSSSTAYMQLSS 85

##### RESULT 2

US-10-932-334-73

```
; Sequence 73, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-73

Query Match          19.0%; Score 115; DB 6; Length 122;
Best Local Similarity 28.7%; Pred. No. 2e-06;
Matches 25; Conservative 19; Mismatches 41; Indels 2; Gaps 1;

QY 19 SRLDCRHEHTSSSNMWFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGYTCALHH 78
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 17 SVKLSCKASGYFTSYMHWVKQPGQGLEWIGRIDPSDYPNNEKFKGKATLT--VDK 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 79 SGHSPPISSQNVTVLRDLKLVKCEGVY 105
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 75 SSTAYMQLSSLTSEDSAVYICASY 101
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :

RESULT 3
US-10-932-334-71
; Sequence 71, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-71

Query Match          18.0%; Score 109; DB 6; Length 120;
Best Local Similarity 31.7%; Pred. No. 8.9e-06;
Matches 32; Conservative 11; Mismatches 42; Indels 16; Gaps 4;

QY 19 SRLDCRHEHTSSSNMWFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGYTCALHH 78
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 17 SVKLSCKASGYFTSYMHWVKQPGQGLEWIGRIDPSDYPNNEKFKGKATLT--VDK 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 79 SGHSPPISSQNVTVLRDLKLVKCEGVY 105
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 75 SSTAYMQLSSLTSEDSAVYICASY 101
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :

RESULT 4
US-10-932-334-72
; Sequence 72, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
; APPLICANT: ImmunoGen, Inc.
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
; FILE REFERENCE: A8689
; CURRENT APPLICATION NUMBER: US/10/932,334
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US/10/729,441
; PRIOR FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: 10/170,390
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody structure
US-10-932-334-72

Query Match          18.0%; Score 109; DB 6; Length 120;
Best Local Similarity 31.7%; Pred. No. 8.9e-06;
Matches 32; Conservative 11; Mismatches 42; Indels 16; Gaps 4;

QY 19 SRLDCRHEHTSSSNMWFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGYTCALHH 78
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 17 SVKLSCKASGYFTSYMHWVKQPGQGLEWIGRIDPSDYPNNEKFKGKATLT--VDK 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 79 SGHSPPISSQNVTVLRDLKLVKCEGVY 111
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 79 STAYMELSS--LTNEDSAVYICTRTDWDYAMDY 109
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :

RESULT 5
US-10-512-184-36
; Sequence 36, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"orderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv SS2 with
; OTHER INFORMATION: specificity against Sclerotinia sclerotiorum;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-36

Query Match          16.7%; Score 101; DB 6; Length 248;
Best Local Similarity 29.0%; Pred. No. 0.00016;
Matches 27; Conservative 15; Mismatches 49; Indels 2; Gaps 1;

QY 19 SRLDCRHEHTSSSNMWFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGYTCALHH 78
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 19 SVKLSCKASGYFTSYMHWVKQPGQGLEWIGALYPGNSDTSYNQKFKGKATLTAVTST 78
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 79 SGHSPPISSQNVTVLRDLKLVKCEGVY 111
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
Db 79 STAYMELSS--LTNEDSAVYICTRTDWDYAMDY 109
   ||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
```

## RESULT 6

US-10-512-184-50  
; Sequence 50, Application US/10512184  
; Publication No. US20050244901A1  
; GENERAL INFORMATION:  
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.  
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant  
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease  
; TITLE OF INVENTION: resistance against fungi  
; FILE REFERENCE: 3581.01US01  
; CURRENT APPLICATION NUMBER: US/10/512,184  
; CURRENT FILING DATE: 2004-10-22  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50  
; LENGTH: 615  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: fusion protein  
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker  
; OTHER INFORMATION: - scfV S82 - cmcy/H186.  
US-10-512-184-50

Query Match 16.7%; Score 101; DB 6; Length 615;  
Best Local Similarity 29.0%; Pred. No. 0.00046;  
Matches 27; Conservative 15; Mismatches 49; Indels 2; Gaps 1;

QY 19 SLRLDCRHEHTSSSNVYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGYTTCALHH 78

Db 360 SVKMSCKASGYFTSYMHVWVQRPGQGLEWIGVPGNSDTSYNQKFKGKAKLTAVTST 419

QY 79 SGHSPPISSQNVTVLRDLKLVKCEGVYRYFDY 111

Db 420 STAYMELSS--LTNEDSAVYYCTRTDWDYANDY 450

## RESULT 7

US-11-108-135-24  
; Sequence 24, Application US/11108135  
; Publication No. US20050260213A1  
; GENERAL INFORMATION:  
; APPLICANT: Koenig, Scott  
; APPLICANT: Veri, Maria Concetta  
; APPLICANT: Tuallon, Nadine  
; APPLICANT: Bonvini, Ezio  
; APPLICANT: Stavenhagen, Jeffrey  
; APPLICANT: Rankin, Christopher  
; TITLE OF INVENTION: FC-gamma-RIIB-specific antibodies and methods of use thereof  
; FILE REFERENCE: 11183-014-999  
; CURRENT APPLICATION NUMBER: US/11/108,135  
; CURRENT FILING DATE: 2005-04-15  
; PRIOR APPLICATION NUMBER: US 60/562,804  
; PRIOR FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: US 60/582,044  
; PRIOR FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: US 60/582,045  
; PRIOR FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: US 60/654,713  
; PRIOR FILING DATE: 2005-02-18  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 121  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized heavy chain variable region  
US-11-108-135-24

Query Match 16.5%; Score 100; DB 7; Length 121;  
Best Local Similarity 32.7%; Pred. No. 8.9e-05;  
Matches 18; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 19 SLRLDCRHEHTSSSNVYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGYT 73  
Db 17 SVKUSCKASGYFTSYMHVWVQRPGQGLEWGVDPDSTYENYNNKFKGRVTMT 71

## RESULT 8

US-10-932-334-87  
; Sequence 87, Application US/10932334  
; Publication No. US20050249728A1  
; GENERAL INFORMATION:  
; APPLICANT: ImmunoGen, Inc.  
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY  
; FILE REFERENCE: A8689  
; CURRENT APPLICATION NUMBER: US/10/932,334  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US/10/729,441  
; PRIOR FILING DATE: 2003-12-08  
; PRIOR APPLICATION NUMBER: 10/170,390  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 87  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-932-334-87

Query Match 16.5%; Score 100; DB 6; Length 123;  
Best Local Similarity 26.0%; Pred. No. 9e-05;  
Matches 27; Conservative 17; Mismatches 40; Indels 20; Gaps 2;

QY 19 SLRLDCRHEHTSSSNVYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGYTTCALHH 78

Db 17 SVKLSCKASGYFTSYMHVWVQRPGQGLEWIGVPGNSDTSYNQKFKGKAKLTIV---- 72

QY 79 SGHSPPISSQNVTVLRDLKLVKCEGVY-----RYTFD 110

Db 73 ----DKSSSTAYMQLSSLTSEDSAVYYPARGRPDYGSSKWTFD 112

## RESULT 9

US-10-932-334-88  
; Sequence 88, Application US/10932334  
; Publication No. US20050249728A1  
; GENERAL INFORMATION:  
; APPLICANT: ImmunoGen, Inc.  
; TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY  
; FILE REFERENCE: A8689  
; CURRENT APPLICATION NUMBER: US/10/932,334  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US/10/729,441  
; PRIOR FILING DATE: 2003-12-08  
; PRIOR APPLICATION NUMBER: 10/170,390  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 88  
; LENGTH: 123  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: humanized EM164 antibody  
US-10-932-334-88

Query Match 16.5%; Score 100; DB 6; Length 123;  
Best Local Similarity 26.0%; Pred. No. 9e-05;  
Matches 27; Conservative 17; Mismatches 40; Indels 20; Gaps 2;

QY 19 SLRLDCRHEHTSSSNVYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGYTTCALHH 78

Db 17 SVKLSCKASGYFTSYMHVWVQRPGQGLEWIGVPGNSDTSYNQKFKGKAKLTIV---- 72



Search completed: December 6, 2005, 10:48:05  
Job time : 5.64111 secs

Db 17 SVKLSCKASGYTFTSYMMHWKQRPQGGLWIGINPNSGRITNNYNEKFKRKATLTV----- 72

QY 79 SGHSPPISSQNTVLRLDKLVKCEGVY-----RYFFD 110

Db 73 ----DKSSSTAYMQLSSLTSDSAVYYPARGRPDYGGSSKWYFD 112

RESULT 14

US-10-932-334-52  
; Sequence 52, Application US/10932334  
; Publication No. US20050249728A1  
; GENERAL INFORMATION:  
; APPLICANT: ImmunoGen, Inc.  
; TITLE OF INVENTION: ANTI-IGF-1 RECEPTOR ANTIBODY  
; FILE REFERENCE: A8689  
; CURRENT APPLICATION NUMBER: US/10/932,334  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US/10/729,441  
; PRIOR FILING DATE: 2003-12-08  
; PRIOR APPLICATION NUMBER: 10/170,390  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 52  
; LENGTH: 143  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-932-334-52

Query Match 16.5%; Score 100; DB 6; Length 143;  
Best Local Similarity 26.0%; Pred. No. 0.00011;  
Matches 27; Conservative 17; Mismatches 40; Indels 20; Gaps 2;  
  
QY 19 SLRLDCRHENTSSNWMHFSLTRETKKHVLFGTIDPADSYTSYNQNFKEGTYTCALHH 78  
Db 36 SVKLSCKASGYTFTSYMMHWKQRPQGGLWIGINPNSGRITNNYNEKFKRKATLTV----- 91  
  
QY 79 SGHSPPISSQNTVLRLDKLVKCEGVY-----RYFFD 110  
Db 92 ----DKSSSTAYMQLSSLTSDSAVYYPARGRPDYGGSSKWYFD 131

RESULT 15

US-10-932-334-57  
; Sequence 57, Application US/10932334  
; Publication No. US20050249728A1  
; GENERAL INFORMATION:  
; APPLICANT: ImmunoGen, Inc.  
; FILE REFERENCE: A8689  
; CURRENT APPLICATION NUMBER: US/10/932,334  
; CURRENT FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US/10/729,441  
; PRIOR FILING DATE: 2003-12-08  
; PRIOR APPLICATION NUMBER: 10/170,390  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 57  
; LENGTH: 98  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-932-334-57

Query Match 16.4%; Score 99; DB 6; Length 98;  
Best Local Similarity 32.7%; Pred. No. 8.9e-05;  
Matches 18; Conservative 14; Mismatches 23; Indels 0; Gaps 0;  
  
QY 19 SLRLDCRHENTSSNWMHFSLTRETKKHVLFGTIDPADSYTSYNQNFKEGTYT 73  
Db 17 SVKLSCKASGYTFTSYMMHWKQRPQGGLWIGINPNSGRITNNYNEKFKRKATLT 71

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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:13 ; Search time 25.9129 Seconds  
(without alignments)  
354.148 Million cell updates/sec

Title: US-10-611-655-4  
Perfect score: 605  
Sequence: 1 QVSRGQKVTSLTACLVDSLS.....VLRDKLVKCEGVYRYFDY 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/prodata/1/1aa/6 COMB.pep.\*  
3: /cgn2\_6/prodata/1/1aa/H COMB.pep.\*  
4: /cgn2\_6/prodata/1/1aa/PCTUS COMB.pep.\*  
5: /cgn2\_6/prodata/1/1aa/RE COMB.pep.\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	424	70.1	161	2 US-09-949-016-11168	Sequence 11168, A
2	242.5	40.1	105	2 US-09-513-999C-4247	Sequence 4247, App
3	126	20.8	120	2 US-10-092-246-12	Sequence 12, Appl
4	126	20.8	120	2 US-10-096-246A-12	Sequence 12, Appl
5	125.5	20.7	119	1 US-08-553-497A-12	Sequence 12, Appl
6	125	20.7	117	2 US-09-065-059-15	Sequence 15, Appl
7	125	20.7	117	2 US-08-913-555-15	Sequence 15, Appl
8	124.5	20.6	116	1 US-08-672-345C-17	Sequence 17, Appl
9	124.5	20.6	116	2 US-09-214-095D-17	Sequence 17, Appl
10	124.5	20.6	116	2 US-09-940-727B-17	Sequence 17, Appl
11	123.5	20.4	119	2 US-08-767-128-6	Sequence 6, Appli
12	123	20.3	113	1 US-08-273-146-59	Sequence 59, Appl
13	123	20.3	113	2 US-09-214-095D-118	Sequence 118, App
14	123	20.3	113	2 US-09-940-727B-118	Sequence 118, App
15	122.5	20.2	111	2 US-08-881-037-14	Sequence 14, Appl
16	122.5	20.2	119	2 US-08-881-037-62	Sequence 62, Appl
17	122.5	20.2	146	2 US-09-069-628-30	Sequence 30, Appl
18	121.5	20.1	119	1 US-08-553-497A-8	Sequence 8, Appli
19	121.5	20.1	119	1 US-08-800-198-2	Sequence 2, Appli
20	121.5	20.1	119	2 US-09-296-595-2	Sequence 2, Appli
21	121.5	20.1	240	1 US-08-800-198-8	Sequence 8, Appli
22	121.5	20.1	240	2 US-09-296-595-8	Sequence 8, Appli
23	121	20.0	98	2 US-08-881-037-59	Sequence 59, Appl
24	120.5	19.9	111	2 US-08-881-037-17	Sequence 17, Appl
25	120.5	19.9	119	2 US-08-881-037-63	Sequence 63, Appl
26	119.5	19.8	111	2 US-08-881-037-16	Sequence 16, Appl
27	119.5	19.8	119	2 US-08-881-037-61	Sequence 61, Appl

28	118	19.5	119	2	US-09-406-532-2	Sequence 2, Appli
29	116	19.2	114	2	US-09-726-219A-226	Sequence 226, App
30	116	19.2	114	2	US-09-196-522-226	Sequence 226, App
31	116	19.2	118	2	US-09-698-705-9	Sequence 9, Appli
32	115.5	19.1	111	2	US-08-881-037-15	Sequence 15, Appl
33	115.5	19.1	119	2	US-08-881-037-60	Sequence 60, Appl
34	114	18.8	116	1	US-08-690-102A-4	Sequence 4, Appli
35	114	18.8	116	2	US-09-121-902-4	Sequence 4, Appli
36	114	18.8	116	2	US-09-155-107-4	Sequence 4, Appli
37	114	18.8	116	4	PCT-US95-09641-4	Sequence 4, Appli
38	113	18.7	256	2	US-09-526-738A-2	Sequence 2, Appli
39	113	18.7	258	2	US-09-526-738A-4	Sequence 4, Appli
40	112	18.5	135	1	US-08-621-751A-12	Sequence 12, Appl
41	112	18.5	142	2	US-09-069-628-27	Sequence 27, Appl
42	112	18.5	241	1	US-08-235-838-11	Sequence 11, Appl
43	112	18.5	241	1	US-08-465-473B-11	Sequence 11, Appl
44	112	18.5	637	1	US-08-235-838-16	Sequence 16, Appl
45	112	18.5	637	1	US-08-465-473B-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-09-949-016-11168  
; Sequence 11168, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11168  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-11168

Query Match 70.1%; Score 424; DB 2; Length 161;  
Best Local Similarity 73.9%; Pred. No. 1.1e-40;  
Matches 88; Conservative 3; Mismatches 12; Indels 16; Gaps 3;  
QY 1 QVSRGQKVTSLTACLVDSLSRDLDCRHENTSSSNYNWHPSLTRETKKHVLFGTTID-PADSY 59  
DB 15 QVSRGQKVTSLTACLVDSLSRDLDCRHENTSSSIQIYEFSLTRETKKHVLFGTGVVEHY 74  
QY 60 TS-----YNNQNF-----KDEGTYTCALHSHGSHSPPISSQNTVTLRDLKLVKCEGV 103  
DB 75 RRTNFTSKYNNKVLVLSAFTSKDEGTYTCALHSHGSHSPPISSQNTVTLRDLKLVKCEGI 133

RESULT 2  
US-09-513-999C-4247  
; Sequence 4247, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C



[illegible]



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; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USF1
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-767-128-6

Query Match 20.4%; Score 123.5; DB 2; Length 119;
Best Local Similarity 32.3%; Pred. No. 1.8e-06;
Matches 30; Conservative 17; Mismatches 43; Indels 3; Gaps 2;

QY 20 LRLDCRHEHTSSSNMWHFSLTRETCKHVLFGTIDPADSYTSYNQNFKDEGYTCALHHS 79
Db 18 VLSKASGYTFTSYMMHWKQRPQGLEWIGRIDPSDSETHYNQKFKDKATLT--VDKS 75

QY 80 GHSPPISQNVTVLRDKLVKCGVYRY--FDY 111
Db 76 SSTAVQLSSLTSSDSAVVYCARHHGYGYAMDY 108

RESULT 12
US-08-723-146-59
; Sequence 59, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.
; TITLE OF INVENTION: The Isolation and Production of
; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IGEN, Inc.
; STREET: 1530 East Jefferson St.
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20852
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/273,146
; FILING DATE: 14-JUL-1994

```

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ryan, John W.
; REGISTRATION NUMBER: 33,771
; REFERENCE/DOCKET NUMBER: 09000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-984-8000
; TELEFAX: 301-230-0158
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-273-146-59

Query Match 20.3%; Score 123; DB 1; Length 113;
Best Local Similarity 31.2%; Pred. No. 1.9e-06;
Matches 29; Conservative 15; Mismatches 47; Indels 2; Gaps 1;

QY 19 SLRLDCRHEHTSSSNMWHFSLTRETCKHVLFGTIDPADSYTSYNQNFKDEGYTCALHH 78
Db 17 SVKMSCKASGYTFTSYMMHWKQRPQGLEWIGYINPSTGYTEYNQKFKDKATLTADKSS 76

QY 79 SGHSPPISQNVTVLRDKLVKCGVYRY--FDY 111
Db 77 STAYMQLSS--LTSEDSAVVYCARHLYYAMDY 107

RESULT 13
US-09-214-095D-118
; Sequence 118, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 118
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-118

Query Match 20.3%; Score 123; DB 2; Length 113;
Best Local Similarity 32.6%; Pred. No. 1.9e-06;
Matches 31; Conservative 18; Mismatches 36; Indels 10; Gaps 3;

QY 19 SLRLDCRHEHTSSSNMWHFSLTRETCKHVLFGTIDPADSYTSYNQNFKDEGYTCALHH 78
Db 16 SVKMSCKASGYTFTSYMMHWKQRPQGLEWIGTIDLSYTYGYNQNFKGRATLT--LDE 73

QY 79 SGHSPPISQNVTVLRDKLVKCGVY--RYTFDY 111
Db 74 SENTAYMQLSSLT-----SEDSAVVYCSRRGFY 102

RESULT 14
US-09-940-727B-118
; Sequence 118, Application US/09940727B
; Patent No. 6913917
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:12 ; Search time 114.094 Seconds  
(without alignments)  
686.395 Million cell updates/sec

Title: US-10-611-655-4  
Perfect score: 605  
Sequence: 1 QVSRGQKVTSLACLVDQSL.....VLRDKLVKCEGVYRYFYD 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	424	70.1	161	1 THY1 HUMAN	P04216 homo sapien
2	418	69.1	161	1 Q5R508 PONPY	Q5R508 pongo pygma
3	417	68.9	161	1 THY1 MACMU	O62643 macaca mula
4	377	62.3	145	1 O59CA0 HUMAN	O59CA0 homo sapien
5	332	54.9	161	2 Q9WRU5 CAVPO	Q9WRU5 cavia porce
6	291.5	48.2	162	1 THY1 MOUSE	P01831 mus musculus
7	291.5	48.2	162	2 Q53YX2 MOUSE	Q53YX2 mus musculus
8	280	46.3	161	1 THY1 RAT	P01830 rattus norv
9	189	31.2	160	2 Q7T252 CHICK	Q7T252 gallus gall
10	176.5	29.2	160	1 THY1 CHICK	Q07212 gallus gall
11	132	21.8	143	2 Q924P9 MOUSE	Q924P9 mus musculus
12	130	21.5	143	2 Q91V67 MOUSE	Q91V67 mus musculus
13	126	20.8	114	2 Q9JL81 MOUSE	Q9JL81 mus musculus
14	118.5	19.6	146	2 Q924R8 MOUSE	Q924R8 mus musculus
15	117	19.3	616	2 Q504M7 MOUSE	Q504M7 mus musculus
16	114.5	18.9	142	2 Q924Q2 MOUSE	Q924Q2 mus musculus
17	113	18.7	617	2 Q4KWL5 MOUSE	Q4KWL5 mus musculus
18	111.5	18.4	481	2 Q91WT3 MOUSE	Q91WT3 mus musculus
19	109	18.0	139	1 HV07 MOUSE	P01751 mus musculus
20	109	18.0	145	2 Q924P8 MOUSE	Q924P8 mus musculus
21	107.5	17.8	140	2 Q924P7 MOUSE	Q924P7 mus musculus
22	105.5	17.4	570	2 Q5B031 BRAKE	Q5B031 brachydanio
23	105	17.4	143	2 Q924Q5 MOUSE	Q924Q5 mus musculus
24	104	17.2	117	1 HV06 MOUSE	P01750 mus musculus
25	103	17.0	117	1 HV05 MOUSE	P01749 mus musculus
26	103	17.0	488	2 Q8K0F2 MOUSE	Q8K0F2 mus musculus
27	102.5	16.9	470	2 Q7TWK1 MOUSE	Q7TWK1 mus musculus
28	102	16.9	137	2 Q924R6 MOUSE	Q924R6 mus musculus
29	102	16.9	145	2 Q924R3 MOUSE	Q924R3 mus musculus
30	102	16.9	146	2 Q924Q3 MOUSE	Q924Q3 mus musculus
31	101	16.7	60	2 Q9XT67 CANPA	Q9XT67 canis famil

32 101 16.7 119 2 Q9GYZ2 MOUSE Q9GYZ2 mus musculus  
33 101 16.7 120 1 HV50 MOUSE P06329 mus musculus  
34 101 16.7 145 2 Q924R4 MOUSE Q924R4 mus musculus  
35 100.5 16.6 144 2 Q924P5 MOUSE Q924P5 mus musculus  
36 100 16.5 117 1 HV49 MOUSE P06328 mus musculus  
37 99.5 16.4 140 2 Q924E2 MOUSE Q924E2 mus musculus  
38 99 16.4 117 1 HV09 MOUSE P01753 mus musculus  
39 99 16.4 141 2 Q924Q4 MOUSE Q924Q4 mus musculus  
40 99 16.4 142 2 Q924Q1 MOUSE Q924Q1 mus musculus  
41 99 16.4 143 2 Q91VA2 MOUSE Q91VA2 mus musculus  
42 99 16.4 143 2 Q924R7 MOUSE Q924R7 mus musculus  
43 99 16.4 143 2 Q924R0 MOUSE Q924R0 mus musculus  
44 99 16.4 145 2 Q924P7 MOUSE Q924P7 mus musculus  
45 99 16.4 145 2 Q924Q6 MOUSE Q924Q6 mus musculus

## ALIGNMENTS

RESULT 1  
ID THY1 HUMAN STANDARD; PRT; 161 AA.  
AC P04216; Q16008; Q9NSP1;  
DT 20-MAR-1987 (Rel. 04, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 10-MAY-2005 (Rel. 47, Last annotation update)  
DE ThY-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90) (CD90 antigen).  
GN Name=THY1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86016759; PubMed=2864690;  
RA Seki T., Spurr N., Obata F., Goyert S., Goodfellow P., Silver J.;  
RT "The human ThY-1 gene: structure and chromosomal location.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:6657-6661(1985).  
RN [2].  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20403900; PubMed=10944468; DOI=10.1006/bbrc.2000.3282;  
RA Ye Z., Connor J.R.;

RT "CDNA cloning by amplification of circularized first strand cDNAs reveals non-IRG-regulated iron-responsive mRNAs.";  
RL Biochem. Biophys. Res. Commun. 275:223-227(2000).  
RN [3].  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Amysdala;  
RG The German cDNA consortium;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RA [4].  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RC TISSUE=Brain, and Eye;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schenker S., White M., Clifton S., Wagner L., Shenmen C.M., Schuler G.D., Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.D., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Dapkinenko L., Marusina K., Farmer A.A., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schenker S., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosch S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalls D.E., Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RP [5]  
RX NUCLEOTIDE SEQUENCE OF 1-55.  
RP MEDLINE:93240114; PubMed:7683034; DOI=10.1094/jem.177.5.1331;  
RA Craig W., Kay R., Cutler R.L., Lansdorff P.M.;  
RA "Expression of Thy-1 on human hematopoietic progenitor cells.";  
RL J. Exp. Med. 177:1331-1342(1993).  
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions  
CC during synaptogenesis and other events in the brain.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)  
CC domain.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC  
CC EMBL; M11749; AAA61180.1; -; Genomic DNA.  
DR EMBL; AF261093; AAG13904.1; -; mRNA.  
DR EMBL; AL161958; CAB82306.1; -; mRNA.  
DR EMBL; BC005175; AAH05175.1; -; mRNA.  
DR EMBL; BC065559; AAH65559.1; -; mRNA.  
DR EMBL; S59749; AAB26353.2; -; mRNA.  
DR PIR; A02106; TDHU.  
DR PIR; T47130; T47130.  
DR Ensembl; ENSG00000154096; Homo sapiens.  
DR HGNC; HGNC:11801; THY1.  
DR H-InvDB; HIX0010195; -.  
DR MIM; 188230; -.  
DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
DR GO; GO:0005886; C:plasma membrane; NAS.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00409; IG; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein;  
KW Membrane; Signal; T-cell.  
FT SIGNAL 1 19  
FT CHAIN 20 130 Thy-1 membrane glycoprotein.  
FT PROPEP 131 161 Removed in mature form.  
FT DOMAIN 20 126 Ig-like V-type.  
FT LIPID 130 130 GPI-anchor amidated cysteine.  
FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 79 79 N-linked (GlcNAc...)  
FT CARBOHYD 119 119 N-linked (GlcNAc...)  
FT CARBOHYD 139 139 By similarity.  
FT DISULFID 28 130 By similarity.  
FT DISULFID 38 104 LT -> AP (in Ref. 5).  
FT CONFLICT 54 55 LT -> H (in Ref. 1).  
FT CONFLICT 85 85 N -> H (in Ref. 1).  
SQ SEQUENCE 161 AA; 17935 MW; 2B6796DA8E7454B CRC64;  
  
Query Match 70.1%; Score 424; DB 1; Length 161;  
Best Local Similarity 73.9%; Pred. No. 8.8e-37;  
Matches 88; Conservative 3; Mismatches 12; Indels 16; Gaps 3;  
  
QY 1 QVSRGQKVTSLTACLVDSLRDCHRENTSSSNVMMHFSLTRETKKHVLFGTID-PADSY 59  
DB 15 QVSRGQKVTSLTACLVDSLRDCHRENTSSSPQIYEFSLTRETKKHVLFGTVGVPETHY 74  
QY 60 TS-----YQNQF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKCEGV 103  
DB 75 RSRNTFTSKYNNKVLVLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKCEGI 133  
  
RESULT 2  
Q5R508\_PONPY  
ID Q5R508\_PONPY PRELIMINARY; PRT; 161 AA.

AC Q5R508;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Hypothetical protein DKFZp459C1015.  
GN Name=DKFZp459C1015;  
OS Pongo pygmaeus (Orangutan).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Pongo.  
OX NCBI\_TaxID=9600;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Cortex;  
RG The German cDNA Consortium;  
RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Weill B., Amid C.,  
RA Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; CR861077; CAH93158.1; -; mRNA.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Hypothetical protein; Immunoglobulin domain.  
SQ SEQUENCE 161 AA; 17963 MW; 2B679DD8CB0401B CRC64;  
  
Query Match 69.1%; Score 418; DB 2; Length 161;  
Best Local Similarity 72.3%; Pred. No. 3.8e-36;  
Matches 86; Conservative 5; Mismatches 12; Indels 16; Gaps 3;  
  
QY 1 QVSRGQKVTSLTACLVDSLRDCHRENTSSSNVMMHFSLTRETKKHVLFGTID-PADSY 59  
DB 15 QVSRGQKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETKKHVLFGTVGVPETHY 74  
QY 60 TS-----YQNQF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKCEGV 103  
DB 75 RSRNTFTSKYNNKVLVLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKCEGI 133  
  
RESULT 3  
THY1\_MACMU  
ID THY1\_MACMU STANDARD; PRT; 161 AA.  
AC 062643;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90  
DE antigen).  
GN Name=THY1;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopitheidae; Cercopitheciniae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Thymus;  
RA Margulies B.J., Clements J.E.;  
RT "Rhesus macaque CD90.";  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions  
CC during synaptogenesis and other events in the brain.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like)  
CC domain.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
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CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC

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DR EMBL; U93310; AAC05640.1; -, mRNA.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein;
KW Membrane; Signal; T-cell.
FT SIGNAL 1 19
FT CHAIN 20 130
FT PROPEP 131 161
FT DOMAIN 20 126
FT LIPID 130 130
FT CARBOHYD 42 42
FT CARBOHYD 79 79
FT CARBOHYD 119 119
FT CARBOHYD 139 139
FT DISULPID 28 130
FT DISULPID 38 104
SQ SEQUENCE 161 AA; 18011 MW; 326B135498BA401B CRC64;

Query Match 68.9%; Score 417; DB 1; Length 161;
Best Local Similarity 72.3%; Pred. No. 4.9e-36;
Matches 86; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLDVQSLRDLRCRHSNTSSNNYMHFSLTRTKKHVLFGTID-PADSY 59
DB 15 QVSRGQKVTSLTACLDVQSLRDLRCRHSNTSSPIQYEFSLTRTKKHVLFGTGVPEHTY 74

QY 60 TS-----YQNQ-----NFKDEGTYTCALHSHGSPPISSQNTVTLRDLKLVKCEGV 103
DB 75 RSRNTFTSKYNMKVLYLSAFTKXDEGTYTCXHLHSHGSPPISSQNTVTLRDLKLVKCEGI 133

RESULT 4
ID Q59GA0 HUMAN PRELIMINARY; PRT; 145 AA.
AC Q59GA0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Thy-1 cell surface antigen variant (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209209; BAD92446.1; -, mRNA.
FT NON TER 1
SQ SEQUENCE 145 AA; 15904 MW; 9DA4BC208DCD5766 CRC64;

Query Match 62.3%; Score 377; DB 2; Length 145;
Best Local Similarity 72.7%; Pred. No. 7.5e-32;
Matches 80; Conservative 2; Mismatches 12; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLDVQSLRDLRCRHSNTSSNNYMHFSLTRTKKHVLFGTID-PADSY 59
DB 31 QVSRGQKVTSLTACLDVQSLRDLRCRHSNTSSPIQYEFSLTRTKKHVLFGTGVPEHTY 90

QY 60 TS-----YQNQ-----KDEGTYTCALHSHGSPPISSQNTVTLR 94
DB 91 RSRNTFTSKYNMKVLYLSAFTKXDEGTYTCXHLHSHGSPPISSQNTVTLR 140

RESULT 5
Q9WUR5_CAVPO
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ID Q9WUR5_CAVPO PRELIMINARY; PRT; 161 AA.
AC Q9WUR5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Thy-1 protein precursor.
GN Name=Thy-1;
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystricognathia; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Schaefer H., Burger R., Otto A., Bartels T.;
RT "Characterization and cloning of guinea pig Thy-1.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ238589; CAB44008.1; -, mRNA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 19
FT CHAIN 20 161
FT CHAIN 20 161
SQ SEQUENCE 161 AA; 17995 MW; 241461D901F80B1B CRC64;

Query Match 54.9%; Score 332; DB 2; Length 161;
Best Local Similarity 60.5%; Pred. No. 5e-27;
Matches 72; Conservative 10; Mismatches 21; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLDVQSLRDLRCRHSNTSSNNYMHFSLTRTKKHVLFGTID-PADSY 59
DB 15 QVSRGQKVTSLTACLDVQSLRDLRCRHSNTTTLPIQYEFSLTRTKKHVLFGTGVPEHAY 74

QY 60 TS-----YQNQ-----KDEGTYTCALHSHGSPPISSQNTVTLRDLKLVKCEGV 103
DB 75 RSRNTFTSKYNMKVLYLSAFTKXDEGTYTCXHLHSHGSPPISSQNTVTLRDLKLVKCEGI 133

RESULT 6
ID THY1_MOUSE STANDARD; PRT; 162 AA.
AC P01831;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90) (CD90 antigen).
GN Name=Thy1; Synonyms=Thy-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=85115360; PubMed=2857501;
RX Seki T., Chang H.-C., Moriuchi T., Denome R., Ploegh H., Silver J.;
RT "A hydrophobic transmembrane segment at the carboxyl terminus of thy-1.";
RL Science 227:649-651(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPED).
RC STRAIN=BALB/c;
RX MEDLINE=86055760; PubMed=2866091;
RA Gignere V., Isebe K.-I., Grosveld F.;
RT "Structure of the murine Thy-1 gene.";
RL EMBO J. 4:2017-2024(1985).
RN [3]
RP NUCLEOTIDE SEQUENCE (THY-1.2 ALLOTYPED).
RP
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AC P01830;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen) (CD90) (CD90 antigen).  
GN Name=Thy1; Synonyms=Thy-1;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86005549; PubMed=2864289;  
RA Seki T., Chang H.-C., Moriuchi T., Denome R., Silver J.;  
RT "Thy-1: a hydrophobic transmembrane segment at the carboxyl terminus";  
RL Fed. Proc. 44:2865-2869 (1985).  
RN [2]  
RP NUCLEOTIDE SEQUENCE OF 1-122.  
RX MEDLINE=83115223; PubMed=6130472;  
RA Moriuchi T., Chang H.-C., Denome R., Silver J.;  
RT "Thy-1 cDNA sequence suggests a novel regulatory mechanism.";  
RL Nature 301:80-82 (1983).  
RN [3]  
RP NUCLEOTIDE SEQUENCE OF 20-161.  
RX MEDLINE=85111162; PubMed=2857477;  
RA Seki T., Moriuchi T., Chang H.-C., Denome R., Silver J.;  
RT "Structural organization of the rat thy-1 gene";  
RL Nature 313:485-487 (1985).  
RN [4]  
RP NUCLEOTIDE SEQUENCE OF 20-161.  
RX MEDLINE=85051865; PubMed=6149956; DOI=10.1016/0014-5793(84)81250-8;  
RA Moriuchi T., Silver J.;  
RT "Rat Thy-1 antigen has a hydrophobic segment at the carboxyl terminus";  
RL FEBS Lett. 178:105-108 (1984).  
RN [5]  
RP PROTEIN SEQUENCE OF 20-130.  
RX MEDLINE=82068190; PubMed=6118137;  
RA Campbell D.G., Gagnon J., Reid K.B.M., Williams A.F.;  
RT "Rat brain Thy-1 glycoprotein. The amino acid sequence, disulphide bonds and an unusual hydrophobic region.";  
RL Biochem. J. 195:15-30 (1981).  
RN [6]  
RP STRUCTURE OF CARBOHYDRATES.  
RX MEDLINE=87275814; PubMed=2886334;  
RA Parekh R.B., Tee A.G.D., Dwek R.A., Williams A.F., Rademacher T.W.;  
RT "Tissue-specific N-glycosylation, site-specific oligosaccharide patterns and lentil lectin recognition of rat Thy-1.";  
RL EMBO J. 6:1233-1244 (1987).  
CC -1- FUNCTION: May play a role in cell-cell or cell-ligand interactions during synaptogenesis and other events in the brain.  
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
CC -1- TISSUE SPECIFICITY: Abundant in lymphoid tissues.  
CC -1- PTM: Glycosylation is tissue specific. Sialylation of N-glycans at Asn-93 in brain and at Asn-42, Asn-93 and Asn-117 in thymus.  
CC -1- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like) domain.  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
CC -----  
CC ENBL; X03152; CAA26931.1; -; Genomic DNA.  
CC ENBL; X03150; CAA26929.1; -; mRNA.  
CC ENBL; X02002; CAA26033.1; -; Genomic DNA.  
CC ENBL; M18002; AAA42243.1; -; mRNA.  
CC ENBL; M10666; AAA42242.1; -; mRNA.  
CC PIR; B45909; TDRT.

DR Ensembl; ENSRNOG00000006604; Rattus norvegicus.  
DR RGD; 3860; Thy1.  
DR GO; GO:0009986; C:cell surface; TAS.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR SMART; SM00409; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Direct protein sequencing; Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein; Membrane;  
KW Pyroglutamate carboxylic acid; Sialic acid; Signal; T-cell.  
FT SIGNAL 1 19  
FT CHAIN 20 130  
FT PROPEP 131 161  
FT DOMAIN 20 126  
FT MOD\_RES 20 20  
FT LIPID 130 130  
FT CARBOHYD 42 42  
FT CARBOHYD 42 42  
FT CARBOHYD 93 93  
FT CARBOHYD 117 117  
FT CARBOHYD 117 117  
FT DISULFID 28 130  
FT DISULFID 38 104  
FT CONFLICT 71 71  
FT SEQUENCE 161 AA; 18172 MW; 3285748F3C2C5AB2 CRC64;  
SQ  
Query Match 46.3%; Score 280; DB 1; Length 161;  
Best Local Similarity 50.4%; Pred. No. 1.6e-21;  
Matches 60; Conservative 16; Mismatches 27; Indels 16; Gaps 3;  
QY 1 QVSRGQKVTSLTACLVDSLRDLDRCHENTSSNYMHPSTRTKGVLEGTID-PADSY 59  
DB 15 QMSRGQRVISLTACLVNQLRLDRCHENTNLPIQHEFSLTRKKHVLSGTLGVPEHTY 74  
QY 60 TS-----YQNQF-----KDEGYTCALHSHGSPPISSQNTVTLRDLKLVKCEGV 103  
DB 75 RSRVNLFSDFRIKVLTLNFTTKDEGYMCELRSVQNTSSNKTINIVIRDLKLVKCGI 133  
RESULT 9  
Q77252 CHICK  
ID Q77252\_CHICK PRELIMINARY; PRT; 160 AA.  
AC Q77252;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE THY1.  
GN Name=THY1;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=14711516; DOI=10.1016/j.pep.2003.10.011;  
RA Mehndiratta P., Walton W.J., Hare J.T., Pulido S., Parthasarathy G., Emmett M.R., Marshall A.G., Logan T.M.;  
RT "Expression, purification, and characterization of avian Thy-1 from Leci mammalian and Tns insect cells.";  
RL Protein Expr. Purif. 33:274-287 (2004).  
ENBL; AV230132; AAP31241.1; -; mRNA.  
DR Ensembl; ENSGALG00000006751; Gallus gallus.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00409; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
KW Immunoglobulin domain.

SQ SEQUENCE 160 AA; 18061 MW; 6DC39D8519540CE6 CRC64;

Query Match 31.2%; Score 189; DB 2; Length 160;  
Best Local Similarity 35.6%; Pred. No. 7.2e-12;  
Matches 42; Conservative 22; Mismatches 38; Indels 16; Gaps 3;

QY 1 QVSRGQKVTSLTACLVDSQSLRLDCHRENTSSNYMWHFSLTRTKKHVLFGTIDPADS-Y 59  
15 QAAHQMIRDLGSLGSLRDCRYENKTSPLTYEFSLTQDKRKHIIQSTISVENY 74

Db

QY 60 TS-----YNQNF--KDEGTYTCALHSHGSPPISSQNVTVLRDKLVKRCG 102  
75 RNRANVTMVKNLVCLYLSHFTTSDEGVNMCCLKATNDYTGNOIKNITVKKLEKCA 132

Db

RESULT 10

THY1\_CHICK STANDARD; PRT; 160 AA.

AC Q07212;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Thy-1 membrane glycoprotein precursor (Thy-1 antigen).  
GN Name=THY1;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RC NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 43-55; 59-79 AND 81-101.  
RX MEDLINE=93061794; PubMed=1359371; DOI=10.1016/0169-328X(92)90180-J;  
RA Downing B.J., Gooley A.A., Gunning P., Cunningham A., Jeffrey P.L.;  
RT "Molecular cloning and primary structure of the avian Thy-1 glycoprotein."  
RL Brain Res. Mol. Brain Res. 14:250-260(1992).  
CC -!- FUNCTION: May play a role in cell-cell or cell-ligand interactions during synaptogenesis and other events in the brain.  
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).  
CC -!- TISSUE SPECIFICITY: Forebrain, cerebellum and tectum.  
CC -!- DEVELOPMENTAL STAGE: It is detected at embryonic day 4 (E4) in forebrain and tectum. There is an increase in levels between E16 and the first few days post-hatch. During E19 to hatch a rapid reduction in the levels is seen with a general increase in expression in adulthood.  
CC -!- PTM: The N-terminus is blocked.  
CC -!- SIMILARITY: Contains 1 Ig-like V-type (immunoglobulin-like) domain.  
CC  
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CC  
CC EMBL; S47368; AAA11899.1; -; mRNA.  
CC EMBL; L14924; AAC42216.1; -; mRNA.  
CC PIR; A48975; A48975.  
CC Ensembl; ENSGALG00000006751; Gallus gallus.  
CC InterPro; IPR003599; I9.  
CC SMART; SM00409; IG; 1.  
CC Direct protein sequencing; Glycoprotein; GPI-anchor;  
KW Immunoglobulin domain; lipoprotein; Membrane;  
KW Pyridolone carboxylic acid; Signal; T-cell.  
FT SIGNAL 1 19 By similarity.  
FT CHAIN 20 129 Thy-1 membrane glycoprotein.  
FT PROPEP 130 160 Removed in mature form (By similarity).  
FT MOD\_RES 20 20 Pyridolone carboxylic acid (By similarity).  
FT LIPID 129 129 GPI-anchor amidated cysteine (By similarity).  
FT

FT CARBOHYD 42 42 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 78 78 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 118 118 N-linked (GlcNAc... ) (Potential).  
FT CARBOHYD 138 138 N-linked (GlcNAc... ) (Potential).  
FT DISULFID 28 129 By similarity.  
FT DISULFID 38 103 By similarity.  
FT DISULFID 76 76 R -> F (in Ref. 1; AA sequence).  
FT CONFLICT 82 82 H -> I (in Ref. 1; AA sequence).  
SQ SEQUENCE 160 AA; 18165 MW; E378D241CC2D4739 CRC64;

Query Match 29.2%; Score 176.5; DB 1; Length 160;  
Best Local Similarity 36.2%; Pred. No. 1.5e-10;  
Matches 42; Conservative 22; Mismatches 35; Indels 17; Gaps 4;

QY 1 QVSRGQKVTSLTACLVDSQSLRLDCHRENTSSNYMWHFSLTRTKKHVLFGTIDPADS-Y 59  
15 QAAHQMIRDLGSLGSLRDCRYENKTSPLTYEFSLTQDKRKHIIQSTISVENY 73

Db

QY 60 TS-----YNQNF--KDEGTYTCALHSHGSPPISSQNVTVLRDKLVK 100  
74 RNRANVTMVKNLVCLYLSHFTTSDEGVNMCCLKATNDYTGNOIKNITVKKLEK 129

Db

RESULT 11

Q924P9\_MOUSE PRELIMINARY; PRT; 143 AA.

AC Q924P9;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE V303-D-J-C mu protein (Fragment).  
GN Name=V303-D-J-C mu;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RC NUCLEOTIDE SEQUENCE.  
RA Kozono Y., Kozono H., Azuma T.;  
RC STRAIN=C57BL/6;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=7523684;  
RA Pokkuluri P.R., Southillier F., Li Y., Kuderova A., Lee J., Cygler M.;  
RT "Preparation, characterization and crystallization of an antibody Fab fragment that recognizes RNA. Crystal structures of native Fab and three Fab-monomononucleotide complexes."  
RT J. Mol. Biol. 243:283-297(1994).  
RL EMBL; AB069916; BAB63932.1; -; mRNA.  
DR PIR; PH1160; PH1160.  
DR PIR; PH1161; PH1161.  
DR PIR; PH1162; PH1162.  
DR PIR; S53751; S53751.  
DR HSP; P01751; IAGW.  
DR Ensembl; ENSMUSG000000061773; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG\_LIKE; 1.  
FT NON\_TER 1 143  
FT NON\_TER 143 143  
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;

Query Match 21.8%; Score 132; DB 2; Length 143;  
Best Local Similarity 28.2%; Pred. No. 7e-06;  
Matches 33; Conservative 12; Mismatches 38; Indels 34; Gaps 2;

QY 19 SLRLDCHRENTSSNYMWHFSLTRTKKHVLFGTIDPADSITYSNQNFK----- 67  
17 SVKLSCASGVTFTSYMWMQVRQPGQGLEWIGEDPSDSTYNYNQKPKGKATLVDTSS 76

Db

```
QY 68 -----DEGTYTCALHSHGSPPISSQNVTVLRDK-----LVKCE 101
DB 77 STAYMQLSLTSDSAVYGCASHYSSDYWGQGTTLTVSSSESQFPNVPFLVSC 133

RESULT 12
Q91V67_MOUSE
ID Q91V67_MOUSE PRELIMINARY; PRT; 143 AA.
AC Q91V67;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE VH186.2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).
GN Name=VH186.2-D-J-C mu; Synonyms=V304-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069912; BAB63928.1; -; mRNA.
DR EMBL; AB069914; BAB63930.1; -; mRNA.
DR PIR; S26744; S26744.
DR HSSP; P01751; 1A6W.
DR SMR; Q91V67; 1-129.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM003596; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15775 MW; 91BC6012B44EPEBF CRC64;

Query Match 21.5%; Score 130; DB 2; Length 143;
Best Local Similarity 33.7%; Pred. No. 1.1e-05;
Matches 31; Conservative 15; Mismatches 44; Indels 2; Gaps 1;

QY 19 SRLDCRHEHTSSSNVHMFSLTRTKKHLVFGTIDPADSYTSYQNFKDEGTYTCALHH 78
DB 17 SVKLSCKAGSYFTSYHMHVQKRPQGLEWIGVIDPSDSTYNYNQKFGKATLTVDTS 76

QY 79 SGHSPPISSQNVTVLRDKLVKCEGVYRYFD 110
DB 77 STAYMQLSS--LTSDSAVYCYCAPTVDDWYFD 106

RESULT 13
Q9JL81_MOUSE
ID Q9JL81_MOUSE PRELIMINARY; PRT; 114 AA.
AC Q9JL81;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c;
RA MEDLINE=20448942; PubMed=1092488;
RX DOI=10.1128/IAI.68.10.5803-5808.2000;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
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RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206025; AAF69323.1; -; mRNA.
DR HSSP; P01751; 1NOB.
DR SMR; Q9JL81; 2-114.
DR Ensembl; ENSMUSG0000021155; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR SMART; SM003596; IG_V.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE68A56F8 CRC64;

Query Match 20.8%; Score 126; DB 2; Length 114;
Best Local Similarity 32.0%; Pred. No. 2.3e-05;
Matches 33; Conservative 11; Mismatches 41; Indels 18; Gaps 2;

QY 19 SRLDCRHEHTSSSNVHMFSLTRTKKHLVFGTIDPADSYTSYQNFKDEGTYTCALHH 78
DB 9 SVKLSCKAGSYFTSYHMHVQKRPQGLEWIGVIDPSDSTYNYNQKFGKATLTVDTS 64

QY 79 SGHSPPISSQNVTVLRDKLVKCEGVYRYFD 111
DB 65 ----DKSSSTAYMQLSSPTSDSAVYCYCAPTVDDWYFD 103

RESULT 14
Q924R8_MOUSE
ID Q924R8_MOUSE PRELIMINARY; PRT; 146 AA.
AC Q924R8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
GN Name=VH186.2-D-J-C mu;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=3135311;
RA Corbet S., Hirn M., Roth C., Theze J., Fougereau M., Schiff C.;
RT "Allogeneic manipulation of the GAT idiotype cascade. Immunization of
RT C57BL/6 mice by BALB/c anti-idiotypes stimulates similar strain-
RT specific V genes as the original antigen.";
RL J. Immunol. 141:779-784(1988).
DR EMBL; AB067781; BAB63266.1; -; mRNA.
DR PIR; F28833; F28833.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
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DR PIR; PH1150; PH1150.  
DR PIR; PH1151; PH1151.  
DR PIR; PH1152; PH1152.  
DR PIR; PH1153; PH1153.  
DR HSSP; P01751; 1A6W.  
DR SNR; Q924R8; 1-137.  
DR Ensembl; ENSMUSG00000021155; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_V.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1  
FT TER 146  
SQ SEQUENCE 146 AA; 16216 MW; 92460F1DFB1B7538 CRC64;  
Query Match 19.6%; Score 118.5; DB 2; Length 146;  
Best Local Similarity 32.3%; Pred. NO. 0.00019;  
Matches 31; Conservative 13; Mismatches 4; Indels 5; Gaps 2;  
QY 19 SRLDRCRHENTSSNWMHFSLTRETKKHLVFGTIDPADSYTSYNQNFKDEGTTCALHH 78  
|::|||:  
DB 17 SVKLCKASGYFTFTSYMMQVKRGLEWIGRIDPSNGGTYKNEFKSKATLTVDKPS 76  
|::|||:  
QY 79 SGHSPPISQNVTVLRLDKLVKCEGVY---RYIFY 111  
|::|||:  
DB 77 STAYMQLS--LTSEDSAVYCARYSGSSLYFYD 110  
|::|||:  
RESULT 15  
Q504M7 MOUSE  
ID Q504M7\_MOUSE PRELIMINARY; PRT; 616 AA.  
AC Q504M7;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Rahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalilus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
RG NIH MGC Project;  
RL Submitted (May-2005) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; BC094936; AAH94936.1; -, mRNA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.

DR PIR; PH1150; PH1150.  
DR PIR; PH1151; PH1151.  
DR PIR; PH1152; PH1152.  
DR PIR; PH1153; PH1153.  
DR HSSP; P01751; 1A6W.  
DR SNR; Q924R8; 1-137.  
DR Ensembl; ENSMUSG00000021155; Mus musculus.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; IG\_V.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG-LIKE; 1.  
FT NON\_TER 1  
FT TER 146  
SQ SEQUENCE 146 AA; 16216 MW; 92460F1DFB1B7538 CRC64;  
Query Match 19.6%; Score 118.5; DB 2; Length 146;  
Best Local Similarity 32.3%; Pred. NO. 0.00019;  
Matches 31; Conservative 13; Mismatches 4; Indels 5; Gaps 2;  
QY 19 SRLDRCRHENTSSNYMHFSLTRETKKHVLFGTIDPADSYTSYNQNFKDEGTTCALHH 78  
|::|||:  
DB 17 SVKLCKASGYFTFTSYMMQVQRPGRGLEWIGRIDPSNGGTYKNEFKSKATLTVDKPS 76  
|::|||:  
QY 79 SGHSPPISQNVTVLRLDKLVKCEGVY---RYIFY 111  
|::|||:  
DB 77 STAYMQLS--LTSEDSAVYCARYSGSSLYFYD 110  
|::|||:  
RESULT 15  
Q504M7 MOUSE  
ID Q504M7\_MOUSE PRELIMINARY; PRT; 616 AA.  
AC Q504M7;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN NUCLEOTIDE SEQUENCE.  
RP RP STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,  
RA Rahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RN NUCLEOTIDE SEQUENCE.  
RP RP STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;  
RG NIH MGC Project;  
RL Submitted (May-2005) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; BC094936; AAH94936.1; -, mRNA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:12 ; Search time 103.652 Seconds  
(without alignments)  
470.529 Million cell updates/sec

Title: US-10-611-655-4  
Perfect score: 605  
Sequence: 1 QVSRQKVTSLTACLVDQSL.....VLRDKLVKCGVYYRYFDY 111

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 43937871 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	605	100.0	111	9	Adw10186 Thy-1 bas
2	424	70.1	161	7	Adp65208 Human Thy
3	424	70.1	161	8	Ab084755 Human can
4	424	70.1	161	9	Adz13572 Human can
5	424	70.1	161	9	Adz13574 Human can
6	424	70.1	161	9	Adz13570 Human can
7	424	70.1	165	3	Aab43939 Human can
8	424	70.1	165	4	Aag73850 Human col
9	422	69.8	161	5	Abb90744 Human Tum
10	422	69.8	161	6	Abu54451 Human Tum
11	419	69.3	368	2	Aay31789 Human Thy
12	402.5	66.5	162	9	Adw10183 Chimeric
13	398	65.8	176	9	Adw10192 Chimeric
14	398	65.8	334	9	Adw10190 Erythrocyt
15	398	65.8	334	9	Adw10188 Chimeric
16	395	65.3	119	2	Aay31787 Human Thy
17	377	62.3	150	8	Adk98542 Human imm
18	291.5	48.2	162	5	Abb90786 Mouse Tum
19	291.5	48.2	162	6	Abu54493 Mouse Tum
20	291.5	48.2	162	8	Ab084754 Murine ca
21	291.5	48.2	162	9	Adz13567 Murine ca
22	291	48.1	171	4	Abg19538 Novel hum
23	280	46.3	161	2	Aaw53480 Rat Thy-1
24	277	45.8	368	2	Aay31788 Rat Thy-1

25	264.5	43.7	114	7	Adf12417	Adf12417	Mouse Thy
26	264.5	43.7	114	8	Adg39435	Adg39435	Mouse Thy
27	256	42.3	119	2	Aay31786	Aay31786	Rat Thy-1
28	242.5	40.1	105	3	Aag00166	Aag00166	Human sec
29	198	32.7	125	2	Aay27074	Aay27074	Monoclonal
30	186.5	30.8	124	9	Adw10184	Adw10184	Human ant
31	162	26.8	51	4	Abg19536	Abg19536	Novel hum
32	143.5	23.7	119	8	Adp79380	Adp79380	Thyrotrop
33	143.5	23.7	124	8	Adp79384	Adp79384	Thyrotrop
34	131	21.7	309	4	Aar70841	Aar70841	SNV-env 1
35	129.5	21.4	118	8	Adu39962	Adu39962	Antibody
36	128.5	21.2	117	1	Aap80148	Aap80148	Biosynthe
37	128.5	21.2	117	1	Aab62295	Aab62295	Sequence
38	128	21.2	98	8	Ados8553	Ados8553	GAP gene
39	128	21.2	116	8	Adm33983	Adm33983	Anti-Nogo
40	128	21.2	116	9	Ady34450	Ady34450	Nogo rece
41	127.5	21.1	117	9	Ady60815	Ady60815	Hybrid pr
42	126.5	20.9	117	8	Adf77173	Adf77173	Anti-VAP-
43	125.5	20.7	119	2	Aar79863	Aar79863	Anti-EGFR
44	125	20.7	117	2	Aaw00831	Aaw00831	Variable
45	125	20.7	117	2	Aaw19017	Aaw19017	Anti-huma

ALIGNMENTS

RESULT 1  
ADW10186  
ID ADW10186 standard; protein; 111 AA.  
XX  
AC ADW10186;  
XX  
DT 24-MAR-2005 (first entry)  
XX  
DE Thy-1 based ThyOx non-immunoglobulin binding polypeptide, SEQ ID 4.  
XX  
KW non-immunoglobulin binding polypeptide; selective binding; ThyOx.  
XX  
OS Synthetic.  
XX  
PN US2004266993-A1.  
XX  
PD 30-DEC-2004.  
XX  
PF 30-JUN-2003; 2003US-00611655.  
XX  
PR 30-JUN-2003; 2003US-00611655.  
XX  
PA (EVAN/) EVANS G A.  
XX  
PI Evans GA;  
XX  
DR WPI; 2005-047648/05.  
XX  
PT New chimeric non-immunoglobulin binding polypeptide comprises  
PT immunoglobulin-like domain containing scaffold and exhibits selective  
PT binding activity, for producing non-immunoglobulin binding polypeptides  
PT with selective binding activity.  
XX  
PS Disclosure; SEQ ID NO 4; 45pp; English.  
XX  
CC The invention relates to a novel chimeric non-immunoglobulin binding  
CC polypeptide. The polypeptide comprises an immunoglobulin-like domain  
CC containing scaffold with two or more solvent exposed loops containing a  
CC different complementarity-determining region (CDR) from a parent antibody  
CC inserted into each of the loops and exhibiting selective binding activity  
CC toward a ligand bound by the parent antibody. The invention further  
CC comprises: a chimeric ThyOx binding polypeptide, comprising one or more  
CC altered immunoglobulin-like domain loop regions of a ThyOx family  
CC polypeptide or at least one immunoglobulin-like domain containing  
CC scaffold derived from a ThyOx family polypeptide, and a heterologous  
CC binding polypeptide exhibiting selective binding activity toward a non-  
CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx





CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA  
 CC nucleic acids. The antibody is useful for detecting the presence or  
 CC absence of cancer cells in an individual which involves contacting cells  
 CC from the individual with the antibody and detecting a complex of a CA  
 CC protein from the cancer cells and the antibody, where the detection of  
 CC the complex correlates with the presence of cancer cells in the  
 CC individual. The composition is useful for inhibiting growth of cancer  
 CC cells in an individual or for delivering a therapeutic agent to cancer  
 CC cells in an individual. The invention is also useful for diagnosing  
 CC cancer, for treating cancer and for inhibiting expression of a CA gene in  
 CC a cell. This sequence represents a human cancer-associated protein of the  
 CC invention.  
 XX Sequence 161 AA;

Query Match 70.1%; Score 424; DB 9; Length 161;  
 Best Local Similarity 73.9%; Pred. No. 1.2e-37;  
 Matches 88; Conservative 3; Mismatches 12; Indels 16; Gaps 3;  
 QY 1 QVSRGQKVTSLTACLVDSLRDCHRENTSSNYMHFSLRTKXKHLFGTID-PADSY 59  
 DB 15 QVSRGQKVTSLTACLVDSLRDCHRENTSSPIQYEFSLRTKXKHLFGTGVPEHTY 74  
 QY 60 TS-----YQNPF-----KDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGV 103  
 DB 75 RSRNTFTSKYNKMKVLYLSAFTSKDSGTTCALHSHSGHSPPISSQNVTVLRDKLVKCEGI 133

RESULT 6  
 ID ADZ13570  
 XX ADZ13570 standard; protein; 161 AA.  
 AC ADZ13570;  
 XX  
 DT 16-JUN-2005 (first entry)  
 XX  
 DE Human cancer-associated protein #328.  
 XX  
 KW Diagnosis; DNA microarray; microarray; biochip; cancer; neoplasm;  
 KW cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2005031001-A2.  
 XX  
 PD 07-APR-2005.  
 XX  
 PF 23-SEP-2004; 2004WO-US031617.  
 XX  
 PR 23-SEP-2003; 2003US-00669920.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 PI Morris DW, Malandro MS;  
 XX  
 DR WPI; 2005-273395/28.  
 XX  
 DR N-PSDB; ADZ13569.  
 XX  
 PT Nucleic acid array useful for detecting cancer associated nucleic acid,  
 PT comprises two or more nucleic acid probes.  
 XX  
 PS Disclosure; SEQ ID NO 1090; 198pp; English.  
 XX

CC The invention relates to a nucleic acid array for detecting a cancer  
 CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.  
 CC The invention also relates to a peptide array comprising two or more  
 CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound  
 CC that binds to a polypeptide, an isolated antibody or its fragment which  
 CC binds to a polypeptide, which is prepared by immunizing a host animal  
 CC with a composition comprising the polypeptide or its antigen binding  
 CC fragment and collecting cells from the host expressing antibodies against  
 CC the antigen or its antigen binding fragment, a composition comprising the  
 CC antibody and a carrier, a method of screening for anticancer activity, a

CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a  
 CC method of treating cancer and a method of inhibiting expression of a CA  
 CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA  
 CC nucleic acids. The antibody is useful for detecting the presence or  
 CC absence of cancer cells in an individual which involves contacting cells  
 CC from the individual with the antibody and detecting a complex of a CA  
 CC protein from the cancer cells and the antibody, where the detection of  
 CC the complex correlates with the presence of cancer cells in the  
 CC individual. The composition is useful for inhibiting growth of cancer  
 CC cells in an individual or for delivering a therapeutic agent to cancer  
 CC cells in an individual. The invention is also useful for diagnosing  
 CC cancer, for treating cancer and for inhibiting expression of a CA gene in  
 CC a cell. This sequence represents a human cancer-associated protein of the  
 CC invention.  
 XX Sequence 161 AA;

Query Match 70.1%; Score 424; DB 9; Length 161;  
 Best Local Similarity 73.9%; Pred. No. 1.2e-37;  
 Matches 88; Conservative 3; Mismatches 12; Indels 16; Gaps 3;  
 QY 1 QVSRGQKVTSLTACLVDSLRDCHRENTSSNYMHFSLRTKXKHLFGTID-PADSY 59  
 DB 15 QVSRGQKVTSLTACLVDSLRDCHRENTSSPIQYEFSLRTKXKHLFGTGVPEHTY 74  
 QY 60 TS-----YQNPF-----KDEGTYTCALHSHSGHSPPISSQNVTVLRDKLVKCEGV 103  
 DB 75 RSRNTFTSKYNKMKVLYLSAFTSKDSGTTCALHSHSGHSPPISSQNVTVLRDKLVKCEGI 133

RESULT 7  
 AAB43939  
 ID AAB43939 standard; protein; 165 AA.  
 XX  
 AC AAB43939;  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Human cancer associated protein sequence SEQ ID NO:1384.  
 XX  
 KW Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; cancer; immunomodulator;  
 KW antidiabetic; antiaesthetic; antirheumatic; antiarthritic; antiviral;  
 KW antiinflammatory; antichryoid; antiallergic; antibacterial; cardiac;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
 KW vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055350-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US005882.  
 XX  
 PR 12-MAR-1999; 99US-0124270P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-587533/55.  
 DR N-PSDB; AAC78148.  
 XX  
 PT Novel isolated nucleic acids comprising sequences encoding peptides  
 PT useful for treating or diagnosing e.g. cancer.  
 XX  
 PS Claim 11; Page 2053-2054; 2352pp; English.  
 XX

CC AAC77607 to AAC78448 encode the human cancer associated proteins given in  
 CC AAB43398 to AAB44239. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; vulnaray; immunomodulator;  
 CC antidiabetic; antiaschmatic; antirheumatic; antiarthritic;  
 CC antinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
 CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention  
 XX

SQ Sequence 165 AA;

Query Match 70.1%; Score 424; DB 3; Length 165;

Best Local Similarity 73.9%; Pred. No. 1.3e-37; Mismatches 12; Indels 16; Gaps 3;  
 Matches 88; Conservative 3;

QY 1 QVSRGQKVTSLTACLVDSLRDLCRHENTSSSNYMHFSLTRTKKHVLFGTID-PADSY 59  
 DB 19 QVSRGQKVTSLTACLVDSLRDLCRHENTSSSPIQYEFSLTRTKKHVLFGTIVGVPHTY 78  
 QY 60 TS-----YNQNF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKCEGV 103  
 DB 79 RSRNTFTSKYNMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKCEGI 137

RESULT 8

AAG73850  
 ID AAG73850 standard; protein; 165 AA.

XX AC AAG73850;

XX DT 03-SEP-2001 (first entry)

XX DE Human colon cancer antigen protein SEQ ID NO:4614.

XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KW colorectal carcinoma; chromosome 11.

XX OS Homo sapiens.

XX PN WO200122920-A2.

XX PD 05-APR-2001.

XX PF 28-SEP-2000; 2000WO-US026524.

XX PR 29-SEP-1999; 99US-0157137P.

XX PR 03-NOV-1999; 99US-0163280P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Birse CB, Rosen CA;

XX WPI; 2001-235357/24.

XX DR N-PSDB; AAB33281.

XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 PT useful for preventing, diagnosing and/or treating colorectal cancers.

XX PS Claim 11; Page 6411-6412; 9803pp; English.

XX

CC AAB32943 to AAB37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
 CC proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene therapy  
 CC and vaccine production. N and P may be used in the prevention, diagnosis  
 CC and treatment of diseases associated with inappropriate P expression. For  
 CC example, N and P may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of P by expressing inactive proteins or to  
 CC supplement the patients own production of P. Additionally, N may be used  
 CC to produce the colon cancer-associated Ps, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the proteins. N and P  
 CC can be used in the prevention, diagnosis and treatment of colorectal  
 CC carcinomas and cancers. AAB37196 to AAB37204 and AAB77789 represent  
 CC sequences used in the exemplification of the present invention. N.B.  
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
 CC to 1052, 7921 and 7922  
 XX

SQ Sequence 165 AA;

Query Match 70.1%; Score 424; DB 4; Length 165;

Best Local Similarity 73.9%; Pred. No. 1.3e-37; Mismatches 12; Indels 16; Gaps 3;  
 Matches 88; Conservative 3;

QY 1 QVSRGQKVTSLTACLVDSLRDLCRHENTSSSNYMHFSLTRTKKHVLFGTID-PADSY 59

DB 19 QVSRGQKVTSLTACLVDSLRDLCRHENTSSSPIQYEFSLTRTKKHVLFGTIVGVPHTY 78

QY 60 TS-----YNQNF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKCEGV 103

DB 79 RSRNTFTSKYNMKVLYLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDLKLVKCEGI 137

RESULT 9

ABB90744

ID ABB90744 standard; protein; 161 AA.

XX AC ABB90744;

XX DT 30-MAY-2002 (first entry)

XX DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 220.

XX KW Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;  
 KW normal endothelial marker; pan-endothelial marker; immunostimulant;  
 KW antiangiogenic; tumour; neoangiogenesis; vascularised tumour;  
 KW polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;  
 KW psoriasis.

XX OS Homo sapiens.

XX PN WO200210217-A2.

XX PD 07-FEB-2002.

XX PF 01-AUG-2001; 2001WO-US024031.

XX PR 02-AUG-2000; 2000US-0222599P.

XX PR 11-AUG-2000; 2000US-0224360P.

XX PR 11-APR-2001; 2001US-0282850P.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI St Croix B, Kinzler KW, Vogelstein B;

XX WPI; 2002-291856/33.

XX DR N-PSDB; ABL92098.

XX An isolated molecule comprising an antibody variable region which  
 PT specifically binds to an extracellular domain of a tumor endothelial  
 PT marker (TEM) protein, useful for inhibiting tumor growth.

XX

PS Claim 35; Page 194; 331pp; English.

XX The invention relates to an isolated molecule comprising an antibody  
CC variable region which specifically binds to an extracellular domain of a  
CC tumour endothelial marker (TEM). The antibodies which bind to TEM  
CC ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM  
CC proteins have cytostatic, immunostimulant and antiangiogenic activity.  
CC They are useful for inhibiting tumour growth, neoangiogenesis in subjects  
CC bearing a vascularised tumour, polycystic kidney disease, diabetic  
CC retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM  
CC genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)  
CC are disclosed, as are marker oligonucleotide sequences: tumour  
CC endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal  
CC endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers  
CC (PEM) ABL91903-ABL91995

XX Sequence 161 AA;

Query Match 69.8%; Score 422; DB 5; Length 161;  
Best Local Similarity 73.3%; Pred. No. 2e-37;  
Matches 88; Conservative 3; Mismatches 11; Indels 18; Gaps 3;  
QY 1 QVSRGQKVTSLTACLVDSLRDCHRENTSSNYMHFSLTRETCKHVLFGTID-PADSY 59  
Db 15 QVSRGQKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKHVLFGTVGPETHY 74  
QY 60 TSYNQNF-----KDEGTYTTCALHSHSGHSPPISSQNVTVLRDKLVKCEGV 103  
Db 75 RS-RTNFTSKYHKVLYLSAFTSKDEGTYTTCALHSHSGHSPPISSQNVTVLRDKLVKCEGI 133

RESULT 10  
ABUS4451  
ID ABUS4451 standard; protein; 161 AA.

XX AC ABUS4451;

XX DT 12-MAR-2003 (first entry)

XX DE Human tumour endothelial marker TEM 13.

XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;  
KW Tumour endothelial marker; normal endothelial marker; PEM;  
KW pan-endothelial marker; polycystic kidney disease; psoriasis;  
KW diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;  
KW neoangiogenesis; immune response; cytostatic; antidiabetic;  
KW ophthalmological; antirheumatic; antiarthritic; antipsoriatic.

XX OS Homo sapiens.

XX PN WO200283874-A2.

XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US008253.

XX PR 11-APR-2001; 2001US-0282850P.

XX PR 06-FEB-2002; 2002US-0354262P.

XX PA (UYJO ) UNIV JOHNS HOPKINS.

XX PI Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;

XX DR WPI; 2003-093016/08.

XX DR N-PSDB; ABX72023.

XX New purified human transmembrane protein, designated as tumor endothelial  
PT marker (TEM) 3, useful for detecting, diagnosing or treating tumors  
PT polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or  
PT psoriasis.

XX PS Disclosure; Page 206-207; 374pp; English.

CC The present invention relates to a novel method for the isolation of  
CC endothelial cells (ECs), and the identification of genes expressed in  
CC normal and tumour ECs. Tumour endothelial marker (TEM), normal  
CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are  
CC identified in human ECs. The human EC marker proteins and the  
CC polynucleotide sequences encoding them are useful for detecting,  
CC diagnosing or treating tumours as well as polycystic kidney disease,  
CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also  
CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for  
CC inducing an immune response to tumour endothelial cells in a patient, or  
CC for identifying candidate drugs for treating tumours. The present  
CC sequence represents a human TEM or NEM protein of the invention  
XX Sequence 161 AA;

Query Match 69.8%; Score 422; DB 6; Length 161;  
Best Local Similarity 73.3%; Pred. No. 2e-37;  
Matches 88; Conservative 3; Mismatches 11; Indels 18; Gaps 3;  
QY 1 QVSRGQKVTSLTACLVDSLRDCHRENTSSNYMHFSLTRETCKHVLFGTID-PADSY 59  
Db 15 QVSRGQKVTSLTACLVDSLRDCHRENTSSPIQYEFSLTRETCKHVLFGTVGPETHY 74  
QY 60 TSYNQNF-----KDEGTYTTCALHSHSGHSPPISSQNVTVLRDKLVKCEGV 103  
Db 75 RS-RTNFTSKYHKVLYLSAFTSKDEGTYTTCALHSHSGHSPPISSQNVTVLRDKLVKCEGI 133

RESULT 11

AAAY31789

XX ID AAY31789 standard; protein; 368 AA.

XX AC AAY31789;

XX DT 17-OCT-2003 (revised)

XX DT 06-DEC-1999 (first entry)

XX DE Human Thy-1-human IgG constant region fusion protein.

XX Thy-1; human; IgG; angiogenesis; cancer; tumour; rheumatoid arthritis;  
KW atherosclerosis; therapy.

XX OS Homo sapiens.

XX OS Chimeric.

XX Key Location/Qualifiers

FT Peptide 1..19 /note= "Thy-1 signal peptide"

FT Protein 18..368 /note= "Thy-1-Ig fusion, specifically claimed in Claim 8"

FT WO9945951-A2.

XX PN 16-SEP-1999.

XX PF 11-MAR-1999; 99WO-US005256.

XX PR 11-MAR-1998; 98US-00077524.

XX PA (HARD ) HARVARD COLLEGE.

XX PA (HABE/) HABER C.

XX PI Haber E, Shaw S, Jain MK, Lee W;

XX DR WPI; 1999-561618/47.

XX DR N-PSDB; AAX87980.

XX PT Inhibiting Thy-1 expression in endothelial cell, useful for inhibiting  
PT angiogenesis.

XX PS Claim 8; Page 46-47; 47pp; English.

XX The present sequence represents a fusion protein, the mature region of

CC which is claimed, comprising the human Thy-1 extracellular region (see  
CC AAY31787) and the constant region (hinge, CH2, CH3) of human IgG1. A  
CC claimed method for inhibiting angiogenesis in a mammal comprises  
CC administering a compound that inhibits Thy-1 associated proliferation of  
CC an endothelial cell. The compound is preferably the extracellular region  
CC of rat or human Thy-1. The method is used in the treatment of a mammal  
CC having a tumour (e.g. by reducing vascularisation), atherosclerosis or  
CC rheumatoid arthritis, the lesions of which may be associated with  
CC neovascularisation (all claimed). Another claimed method for inhibiting  
CC angiogenesis involves administering a Thy-1 antisense nucleic acid or a  
CC Thy-1-specific antibody linked to a cytotoxic agent. A method for  
CC promoting angiogenesis involves administering a compound that increases  
CC Thy-1 expression in an endothelial cell such as a chimeric protein  
CC comprising the Thy-1 extracellular fragment and the constant region of an  
CC immunoglobulin. (Updated on 17-OCT-2003 to standardise OS field)  
xx  
Sequence 368 AA:  
SO  
SO

```

Query Match      69.3%; Score 419; DB 2; Length 368;
Best Local Similarity 73.9%; Pred. No. 1.2e-36;
Matches 88; Conservative 2; Mismatches 11; Indels 18; Gaps 3;

Qy 1 QVSRGQKVTSLTACLVDQSLDRCRHENTSSNNTWMPFLTRTKKGVLFCTID-PADSY 59
      |||||
Db 15 QVSRGQKVTSLTACLVDQSLDRCRHENTSSSPIQYRPSLTRTKKGVLFCTVGVPEHTY 74
      |||||

Qy 60 TSYNQNF-----KDEGYTTCALHSHSGHSPPISSONVTVLRDKLKVCBG 102
      |||
Db 75 RS-RTNFTSKYHKMVLISAFTSKDEGYTTCALHSHSGHSPPISSONVTVLRDKLKVCBG 132

```

RESULT 12	
ADW10183	
ID	ADW10183 standard; protein; 162 AA.
XX	
XX	
AC	ADW10183;
XX	
DT	24-MAR-2005 (first entry)
XX	
XX	
DE	Human Thy-1 protein.
XX	
XX	
KW	non-immunoglobulin binding polypeptide; selective binding; Thy-1.

altered immunoglobulin-like domain loop regions of a ThyOx family polypeptide or at least one immunoglobulin-like domain containing scaffold derived from a ThyOx family polypeptide, and a heterologous binding polypeptide exhibiting selective binding activity toward a non-ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx binding polypeptide above. The chimeric non-immunoglobulin binding polypeptide is useful for producing non-immunoglobulin binding polypeptides having selective binding activity toward a predetermined molecule. This sequence represents a human Thy-1 protein of the invention.

Query Match	66.5%	Score 402.5;	DB 9;	Length 162;
Best Local Similarity	71.9%;	Pred. No. 2.6e-35;		
Matches	87;	Conservative	12;	Indels 19;
Matches	3;	Mismatches	19;	Gaps

Qy	1	QVSRGQVTSLTACLVDSURLDCRHSNTSSNNVMMHFSLTRETYSKVLFGTID-PADSY	59
Db	15	QVSRGQVTSLTACLVDSURLDCRHSNTSSNPQYEESLTRETYSKVLFGTVGPEHTY	74
Qy	60	TSYNQNF-----KDEGTYTCALHSHGSPPI-SSQNVTVLRDLVKCEG	102
Db	75	RS-RTNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHGSPPISSQNVTVLRDLVKCEG	133
Qy	103	V 103	
		:	
Db	134	I 134	

RESULT 13	
ADW10192	
ID	ADW10192 standard; protein; 176 AA.
XX	
XX	
AC	ADW10192;
XX	
XX	
DT	24-MAR-2005 (first entry)
XX	
DE	Chimeric ThyOx carrier containing glucagon-like peptide 1.
XX	
XX	
KW	non-immunoglobulin binding polypeptide; selective binding; ThyOx;
KW	glucagon-like peptide 1; GLP-1.
KW	

XX  
PS Disclosure: SEO ID NO 10: 45pp: English:

CC toward a ligand bound by the parent antibody. The invention further  
 CC comprises: a chimeric ThyOx binding polypeptide, comprising one or more  
 CC altered immunoglobulin-like domain loop regions of a ThyOx family  
 CC polypeptide or at least one immunoglobulin-like domain containing  
 CC scaffold derived from a ThyOx family polypeptide, and a heterologous  
 CC binding polypeptide exhibiting selective binding activity toward a non-  
 CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx  
 CC binding polypeptide above. The chimeric non-immunoglobulin binding  
 CC polypeptide is useful for producing non-immunoglobulin binding  
 CC polypeptides having selective binding activity toward a predetermined  
 CC molecule. This sequence represents a chimeric ThyOx carrier containing  
 CC glucagon-like peptide 1 of the invention.  
 XX  
 SQ Sequence 176 AA;

Query Match 65.8%; Score 398; DB 9; Length 176;  
 Best Local Similarity 72.2%; Pred. No. 9e-35;  
 Matches 83; Conservative 3; Mismatches 11; Indels 18; Gaps 3;  
 QY 6 QKVTSLTACLVDQSLRDCRHSNTSSNNYMHFSLTRTKKHVLFGTID-PADSYTSYNQ 64  
 DB 49 QKVTSLTACLVDQSLRDCRHSNTSSNPQYEFSLTRTKKHVLFGTGVPEHTYRS-RT 107  
 QY 65 NF-----KDEGTYTCALHSHSGHSPPISSQNVTVLRDLKLVKCEGV 103  
 DB 108 NFKSYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDLKLVKCEGI 162

RESULT 14  
 ADM10190  
 ID ADM10190 standard; protein; 334 AA.  
 XX  
 AC ADM10190;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Erythropoietin protein, named SuperEpo.  
 XX  
 KW non-immunoglobulin binding polypeptide; selective binding; ThyOx;  
 KW erythropoietin; SuperEpo.  
 XX  
 OS Chimeric.  
 OS Synthetic.  
 XX  
 PN US2004266993-A1.  
 XX  
 PD 30-DEC-2004.  
 XX  
 PF 30-JUN-2003; 2003US-00611655.  
 XX  
 PR 30-JUN-2003; 2003US-00611655.  
 XX  
 PA (EVAN/) EVANS G A.  
 XX  
 PI Evans GA;  
 XX  
 DR WPI; 2005-047648/05.  
 DR N-PSDB; ADM10189.  
 XX  
 PT New chimeric non-immunoglobulin binding polypeptide comprises  
 PT immunoglobulin-like domain containing scaffold and exhibits selective  
 PT binding activity, for producing non-immunoglobulin binding polypeptides  
 PT with selective binding activity.  
 XX  
 PS Disclosure; SEQ ID NO 8; 45pp; English.

XX The invention relates to a novel chimeric non-immunoglobulin binding  
 CC polypeptide. The polypeptide comprises an immunoglobulin-like domain  
 CC containing scaffold with two or more solvent exposed loops containing a  
 CC different complementarity-determining region (CDR) from a parent antibody  
 CC inserted into each of the loops and exhibiting selective binding activity  
 CC toward a ligand bound by the parent antibody. The invention further  
 CC comprises: a chimeric ThyOx binding polypeptide, comprising one or more  
 CC altered immunoglobulin-like domain loop regions of a ThyOx family  
 CC polypeptide or at least one immunoglobulin-like domain containing

CC altered immunoglobulin-like domain loop regions of a ThyOx family  
 CC polypeptide or at least one immunoglobulin-like domain containing  
 CC scaffold derived from a ThyOx family polypeptide, and a heterologous  
 CC binding polypeptide exhibiting selective binding activity toward a non-  
 CC ThyOx ligand; and a nucleic acid encoding the non-immunoglobulin or ThyOx  
 CC binding polypeptide above. The chimeric non-immunoglobulin binding  
 CC polypeptide is useful for producing non-immunoglobulin binding  
 CC polypeptides having selective binding activity toward a predetermined  
 CC molecule. This sequence represents an erythropoietin protein, named  
 CC SuperEpo, of the invention.  
 XX  
 SQ Sequence 334 AA;

Query Match 65.8%; Score 398; DB 9; Length 334;  
 Best Local Similarity 72.2%; Pred. No. 2e-34;  
 Matches 83; Conservative 3; Mismatches 11; Indels 18; Gaps 3;  
 QY 6 QKVTSLTACLVDQSLRDCRHSNTSSNNYMHFSLTRTKKHVLFGTID-PADSYTSYNQ 64  
 DB 207 QKVTSLTACLVDQSLRDCRHSNTSSNPQYEFSLTRTKKHVLFGTGVPEHTYRS-RT 265  
 QY 65 NF-----KDEGTYTCALHSHSGHSPPISSQNVTVLRDLKLVKCEGV 103  
 DB 266 NFKSYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRDLKLVKCEGI 320

RESULT 15  
 ADM10188  
 ID ADM10188 standard; protein; 334 AA.  
 XX  
 AC ADM10188;  
 XX  
 DT 24-MAR-2005 (first entry)  
 XX  
 DE Chimeric ThyOx carrier containing erythropoietin.  
 XX  
 KW non-immunoglobulin binding polypeptide; selective binding; ThyOx;  
 KW erythropoietin.  
 XX  
 OS Chimeric.  
 OS Synthetic.  
 XX  
 PN US2004266993-A1.  
 XX  
 PD 30-DEC-2004.  
 XX  
 PF 30-JUN-2003; 2003US-00611655.  
 XX  
 PR 30-JUN-2003; 2003US-00611655.  
 XX  
 PA (EVAN/) EVANS G A.  
 XX  
 PI Evans GA;  
 XX  
 DR WPI; 2005-047648/05.  
 DR N-PSDB; ADM10187.  
 XX  
 PT New chimeric non-immunoglobulin binding polypeptide comprises  
 PT immunoglobulin-like domain containing scaffold and exhibits selective  
 PT binding activity, for producing non-immunoglobulin binding polypeptides  
 PT with selective binding activity.  
 XX  
 PS Disclosure; SEQ ID NO 6; 45pp; English.

XX The invention relates to a novel chimeric non-immunoglobulin binding  
 CC polypeptide. The polypeptide comprises an immunoglobulin-like domain  
 CC containing scaffold with two or more solvent exposed loops containing a  
 CC different complementarity-determining region (CDR) from a parent antibody  
 CC inserted into each of the loops and exhibiting selective binding activity  
 CC toward a ligand bound by the parent antibody. The invention further  
 CC comprises: a chimeric ThyOx binding polypeptide, comprising one or more  
 CC altered immunoglobulin-like domain loop regions of a ThyOx family  
 CC polypeptide or at least one immunoglobulin-like domain containing



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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	424	70.1	161	2	T47130	hypothetical prote
2	422	69.8	161	1	TDHU	Thy-1 membrane gly
3	291.5	48.2	162	1	TDMS	Thy-1 membrane gly
4	280	46.3	161	1	TDRT	Thy-1 membrane gly
5	176.5	29.2	160	2	DA8975	Thy-1 glycoprotein
6	132	21.8	111	2	S25048	Ig heavy chain V r
7	130	21.5	111	2	S25045	Ig heavy chain V r
8	129	21.3	116	2	S53751	antibody Fab Jel 1
9	126.5	20.9	120	2	S25175	Ig heavy chain V r
10	126	20.8	120	2	S41394	Ig heavy chain V r
11	124	20.5	69	2	S25150	Ig heavy chain V r
12	123	20.3	106	2	S25036	Ig heavy chain V r
13	122.5	20.2	123	2	S20646	Ig heavy chain V r
14	122	20.2	98	2	PH1164	Ig heavy chain V r
15	122	20.2	111	2	S25054	Ig heavy chain V r
16	122	20.2	111	2	S25052	Ig heavy chain V r
17	121	20.0	98	2	PH1160	Ig heavy chain V r
18	120	19.8	111	2	S25032	Ig heavy chain V r
19	120	19.8	111	2	S26463	Ig heavy chain V r
20	120	19.8	139	2	PS0024	Ig heavy chain pre
21	119	19.7	102	2	S25025	Ig heavy chain - m
22	119	19.7	106	2	PH1005	Ig heavy chain V r
23	119	19.7	111	2	S25024	Ig heavy chain V r
24	118.5	19.6	109	2	S26318	Ig heavy chain V r
25	118	19.5	109	2	S25038	Ig heavy chain V r
26	118	19.5	111	2	S25055	Ig heavy chain V r
27	117	19.3	111	2	S25033	Ig heavy chain V r
28	117	19.3	111	2	S25034	Ig heavy chain V r
29	116	19.2	87	2	PH1162	Ig heavy chain V r

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein; thymocyte; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-161/Product: Thy-1 membrane glycoprotein #status predicted <MAT>  
F:20-141/Domain: extracellular #status predicted <EX1>  
F:31-106/Domain: immunoglobulin homology <IMM>  
F:142-161/Domain: transmembrane #status predicted <TMW>  
F:42,119,139/Binding site: carbohydrate (Aan) (covalent) #status predicted

Query Match 69.8%; Score 422; DB 1; Length 161;  
Best Local Similarity 73.3%; Pred. No. 3.3e-34;  
Matches 88; Conservative 3; Mismatches 11; Indels 18; Gaps 3;

QY 1 QVSRGQKVTSLTACLVDSQSLRDLCDCHRENTSSSNYMHPSLTRETKKHVLFGTID-PADSY 59  
Db 15 QVSRGQKVTSLTACLVDSQSLRDLCDCHRENTSSSPIQVEFSLTRETKKHVLFQVGVPEHTY 74

QY 60 TSYNQF-----KDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCGV 103  
Db 75 RS-RNFTSKYHMKVLYLSAFTSKDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCGI 133

RESULT 3

TDMS  
Thy-1 membrane glycoprotein precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jul-1982 #sequence\_revision 28-May-1986 #text\_change 09-Jul-2004  
C:Accession: A94278; A24647; A94265; I59028; I55957; A03108  
R:Seki, T.; Chang, H.C.; Moriuchi, T.; Denome, R.; Ploegh, H.; Silver, J.  
Science 227, 649-651, 1985  
A:Title: A hydrophobic transmembrane segment at the carboxyl terminus of Thy-1.  
A:Reference number: A94278; MUID:85115360; PMID:2857501  
A:Accession: A94278  
A:Molecule type: DNA  
A:Residues: 1-162 <SIG>  
A:Cross-references: UNIPROT:P01831; UNIPARC:UPI000002395E; GB:M10246; NID:G202032; PIDN:EMBO J. 4, 2017-2024, 1985  
R:Guiguerre, V.; Isobe, K.I.; Grosveld, F.  
A:Title: Structure of the murine Thy-1 gene.  
A:Reference number: A24647; MUID:86055760; PMID:2866091  
A:Contents: Thy-1.2 allotype  
A:Accession: A24647  
A:Molecule type: DNA  
A:Residues: 1-162 <GIG>  
A:Cross-references: UNIPARC:UPI000002395E  
A:Experimental source: strain BALB/c  
R:Williams, A.F.; Gagnon, J.  
Science 216, 696-703, 1982  
A:Title: Neuronal cell Thy-1 glycoprotein: homology with immunoglobulin.  
A:Reference number: A94265; MUID:82199396; PMID:6177036  
A:Accession: A94265  
A:Molecule type: protein  
A:Residues: 20-131 <WIL>  
A:Cross-references: UNIPARC:UPI0000173745  
A>Note: the Thy-1.1 sequence differs from that shown in having 108-Arg  
R:Chang, H.  
Proc. Natl. Acad. Sci. U.S.A. 82, 3819-3823, 1985  
A:Title: Isolation and characterization of mouse Thy-1 genomic clones.  
A:Reference number: I59028; MUID:85216583; PMID:2582427  
A:Accession: I59028  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-162 <RES>  
A:Cross-references: UNIPARC:UPI000002395E; GB:M11160; NID:G202034; PIDN:AAA40441.1; PID:R:Ingraham, H.A.; Lawless, G.M.; Evans, G.A.  
J. Immunol. 136, 1482-1489, 1986  
A:Title: The mouse Thy-1.2 glycoprotein gene: Complete sequence and identification of an  
A:Reference number: I55957; MUID:86113437; PMID:2868059  
A:Accession: I55957  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-162 <RE2>  
A:Cross-references: UNIPARC:UPI000002395E; GB:M12379; NID:G202040; PIDN:AAA40443.1; PID:

C:Comment: The Thy-1.2 sequence is shown.  
C:Genetics:  
A:Map position: 9  
A:Introns: 13/1; 126/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein; pyroglutamic acid; T-cell; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-162/Product: Thy-1 membrane glycoprotein #status predicted <MAT>  
F:31-107/Domain: immunoglobulin homology <IMM>  
F:143-162/Domain: transmembrane #status predicted <TMW>  
F:20/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer  
F:28-131,38-105/Disulfide bonds: #status experimental  
F:42,94,118/Binding site: carbohydrate (Aan) (covalent) #status experimental

Query Match 48.2%; Score 291.5; DB 1; Length 162;  
Best Local Similarity 55.8%; Pred. No. 2e-21;  
Matches 67; Conservative 13; Mismatches 23; Indels 17; Gaps 5;

QY 1 QVSRGQKVTSLTACLVDSQSLRDLCDCHRENTSSSNYMMH-PSLTRETKKHVLFGTID-PADS 58  
Db 15 QVSRGQKVTSLTACLVDSQSLRDLCDCHRENTKDNSIQHFEFSLTREKRVLSGTIGIPEHT 74

QY 59 Y-----TSYNQ-----NF--KDEGTYTCALHSHSGHSPPISSQNVTVLRLDKLVKCGV 103  
Db 75 YRSRVTLNQPIKIVLTLANFTTKDEGDYFCELVQSGANPMSSNKSISVYRDKLVKCGI 134

RESULT 4

TDRT  
thy-1 membrane glycoprotein precursor - rat  
A:Alternate names: thy-1 antigen  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 29-Jun-1981 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: B45909; A45909; A25255; A21652; A90311; A93296; A02107  
R:Seki, T.; Moriuchi, T.; Chang, H.C.; Denome, R.; Silver, J.  
Nature 313, 485-487, 1985  
A:Title: Structural organization of the rat thy-1 gene.  
A:Reference number: A45909; MUID:85111162; PMID:2857477  
A:Accession: B45909  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-161 <SEK>  
A:Cross-references: UNIPROT:P01830; UNIPARC:UPI0000136P21; GB:X02002; NID:G57363; PIDN:A:Accession: A45909  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 20-161 <SE2>  
R:Seki, T.; Chang, H.C.; Moriuchi, T.; Denome, R.; Silver, J.  
Fed. Proc. 44, 2865-2869, 1985  
A:Title: Thy-1: a hydrophobic transmembrane segment at the carboxyl terminus.  
A:Reference number: A25255; MUID:86005549; PMID:2864289  
A:Accession: A25255  
A:Molecule type: DNA  
A:Residues: 1-70,'72-161 <SE3>  
A:Cross-references: UNIPARC:UPI00000170B3E; GB:X03152; NID:G57357; PIDN:CAA26931.1; PID:R:Moriuchi, T.; Silver, J.  
FEBS Lett. 178, 105-107, 1984  
A:Title: Rat Thy-1 antigen has a hydrophobic segment at the carboxyl terminus.  
A:Reference number: A21652; MUID:85051865; PMID:6149956  
A:Accession: A21652  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 20-161 <MOR>  
R:Campbell, D.G.; Gagnon, J.; Reid, K.B.M.; Williams, A.F.  
Biochem. J. 195, 15-30, 1981  
A:Title: Rat brain Thy-1 glycoprotein. The amino acid sequence, disulphide bonds and an  
A:Reference number: A90311; MUID:82068190; PMID:6118137  
A:Accession: A90311  
A:Molecule type: protein  
A:Residues: 20-130 <CAM>  
A:Cross-references: UNIPARC:UPI00000173743

A>Note: this sequence shows homologies with immunoglobulin domains  
 R:Moriuchi, T.; Chang, H.C.; Denome, R.; Silver, J.  
 Nature 301, 80-82, 1983  
 A>Title: Thy-1 cDNA sequence suggests a novel regulatory mechanism.  
 A:Reference number: A93296; MUID:83115223; PMID:6130472  
 A:Accession: A93296  
 A:Molecule type: mRNA  
 A:Residues: 1-122 <MO2>  
 A:Cross-references: UNIPARC:UPI0000173744  
 C:Comment: This glycoprotein is a major constituent of brain-cell membrane and is abundant in the brain.  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: glycoprotein; membrane protein; pyroglyutamic acid  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-130/Product: thy-1 membrane glycoprotein #status experimental <MAT>  
 F:31-106/Domain: immunoglobulin homology <IMM>  
 F:20/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experimental  
 F:28-130,38-104/Disulfide bonds: #status experimental  
 F:42,93,117/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 46.3%; Score 280; DB 1; Length 161;  
 Best Local Similarity 50.4%; Pred. No. 2.7e-20;  
 Matches 60; Conservative 16; Mismatches 27; Indels 16; Gaps 3;  
 QY 1 QVSRGQVTSLSACLVDSQSLRDCHRENTSSSNVMMHPSLRTRETKKHVLFGTID-PADSY 59  
 DB 15 QMSRGQVLSLACLVDSQSLRDCHRENTSSSNVMMHPSLRTRETKKHVLSGLVGEPTY 74  
 QY 60 TS-----YNQNF-----KDEGTYTCALHSHGSPPISSQNVTVLRDLKLVCEGV 103  
 DB 75 RSRVNLFSRDFIKVTLANFTTKDEGYMCELRSVQNPSSNKTINVRDLKLVKCGGI 133

RESULT 5  
 A48975  
 Thy-1 glycoprotein - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C:Accession: A48975  
 R:Dowsing, B.J.; Gooley, A.A.; Gunning, P.; Cunningham, A.; Jeffrey, P.L.  
 Brain Res. Mol. Brain Res. 14, 250-260, 1992  
 A>Title: Molecular cloning and primary structure of the avian Thy-1 glycoprotein.  
 A:Reference number: A48975; MUID:93061794; PMID:1359371  
 A:Accession: A48975  
 A>Status: preliminary  
 A:Molecule type: mRNA; protein  
 A:Residues: 1-160 <DOW>  
 A:Cross-references: UNIPROT:Q07212; UNIPARC:UPI0000136F1D; GB:L14924; NID:G289826; PIDN:  
 A>Note: sequence extracted from NCBI backbone (NCBI:117489, NCBI:117490)  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: glycoprotein

Query Match 29.2%; Score 176.5; DB 2; Length 160;  
 Best Local Similarity 36.2%; Pred. No. 3.7e-10;  
 Matches 42; Conservative 22; Mismatches 35; Indels 17; Gaps 4;  
 QY 1 QVSRGQVTSLSACLVDSQSLRDCHRENTSSSNVMMHPSLRTRETKKHVLFGTID-PADSY 59  
 DB 15 QAAHCQMRDLSACLVDSQSLRDCHRENTSSSNVMMHPSLRTRETKKHVLSGLVGEPTY 73  
 QY 60 TS-----YNQNF-----KDEGTYTCALHSHGSPPISSQNVTVLRDLKLVK 100  
 DB 74 RNRANVTMKNLVCLYLSHTTSDEGYMCELKATNDYTGQIKNITVICKLEKC 129

RESULT 6  
 S25048  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 25-Feb-1994 #sequence\_revision 01-Dec-1995 #text\_change 20-Jun-2000  
 C:Accession: S25048; S25046; S25049  
 R:Jacob, J.; Kelsoe, G.  
 submitted to the EMBL Data Library, July 1992  
 A>Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl)

Query Match 21.5%; Score 130; DB 2; Length 111;  
 Best Local Similarity 33.3%; Pred. No. 8.8e-06;  
 Matches 31; Conservative 13; Mismatches 47; Indels 2; Gaps 1;  
 QY 19 SLRLDCRHEHTSSSNVMMHPSLRTRETKKHVLFGTID-PADSYTSYNQNFKDEGTYTCALHH 78  
 DB 13 SVKLSCKASGYTFTSWMHVVKQPCRGLEWIGRIDPNSGGTKYNEKFSKATLTVDKPS 72  
 QY 79 SGHSPPPISSQNVTVLRDLKLVCEGVYRYFYDY 111  
 DB 73 STACMQLSS--LTSEDSAVVYCARYYVYFYDY 103

RESULT 7  
 S25045  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 25-Feb-1994 #sequence\_revision 01-Dec-1995 #text\_change 20-Jun-2000  
 C:Accession: S25045  
 R:Jacob, J.; Kelsoe, G.  
 submitted to the EMBL Data Library, July 1992  
 A>Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl)

Query Match 21.5%; Score 130; DB 2; Length 111;  
 Best Local Similarity 33.3%; Pred. No. 8.8e-06;  
 Matches 31; Conservative 13; Mismatches 47; Indels 2; Gaps 1;  
 QY 19 SLRLDCRHEHTSSSNVMMHPSLRTRETKKHVLFGTID-PADSYTSYNQNFKDEGTYTCALHH 78  
 DB 13 SVKLSCKASGYTFTSWMHVVKQPCRGLEWIGRIDPNSGGTKYNEKFSKATLTVDKPS 72  
 QY 79 SGHSPPPISSQNVTVLRDLKLVCEGVYRYFYDY 111  
 DB 73 STACMQLSS--LTSEDSAVVYCARYYVYFYDY 103

RESULT 8  
 S53751  
 antibody Fab Jcl 103 heavy chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 31-Dec-2004  
 C:Accession: S53751  
 R:Pokkuluri, P.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.  
 J. Mol. Biol. 243, 283-297, 1994

A:Reference number: S25024  
 A:Accession: S25048  
 A>Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-111 <JAC1>  
 A:Cross-references: UNIPARC:UPI000011609E; EMBL:X67349; NID:G50898; PIDN:CAA47764.1; PTI:  
 A:Accession: S25046  
 A>Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-111 <JAC2>  
 A:Cross-references: UNIPARC:UPI000011609E; EMBL:X67346; NID:G50894; PIDN:CAA47761.1; PTI:  
 A:Accession: S25049  
 A>Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-97, 'GSSL', 102-111 <JAC3>  
 A:Cross-references: UNIPARC:UPI00001160A0; EMBL:X67350; NID:G50900; PIDN:CAA47765.1; PTI:  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 21.8%; Score 132; DB 2; Length 111;  
 Best Local Similarity 33.3%; Pred. No. 5.6e-06;  
 Matches 31; Conservative 13; Mismatches 47; Indels 2; Gaps 1;  
 QY 19 SLRLDCRHEHTSSSNVMMHPSLRTRETKKHVLFGTID-PADSYTSYNQNFKDEGTYTCALHH 78  
 DB 13 SVKLSCKASGYTFTSWMHVVKQPCRGLEWIGRIDPNSGGTKYNEKFSKATLTVDKPS 72  
 QY 79 SGHSPPPISSQNVTVLRDLKLVCEGVYRYFYDY 111  
 DB 73 STAYMQLSS--LTSEDSAVVYCARYYVYFYDY 103

RESULT 7  
 S25045  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 25-Feb-1994 #sequence\_revision 01-Dec-1995 #text\_change 20-Jun-2000  
 C:Accession: S25045  
 R:Jacob, J.; Kelsoe, G.  
 submitted to the EMBL Data Library, July 1992  
 A>Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl)

Query Match 21.5%; Score 130; DB 2; Length 111;  
 Best Local Similarity 33.3%; Pred. No. 8.8e-06;  
 Matches 31; Conservative 13; Mismatches 47; Indels 2; Gaps 1;  
 QY 19 SLRLDCRHEHTSSSNVMMHPSLRTRETKKHVLFGTID-PADSYTSYNQNFKDEGTYTCALHH 78  
 DB 13 SVKLSCKASGYTFTSWMHVVKQPCRGLEWIGRIDPNSGGTKYNEKFSKATLTVDKPS 72  
 QY 79 SGHSPPPISSQNVTVLRDLKLVCEGVYRYFYDY 111  
 DB 73 STACMQLSS--LTSEDSAVVYCARYYVYFYDY 103

RESULT 8  
 S53751  
 antibody Fab Jcl 103 heavy chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 23-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 31-Dec-2004  
 C:Accession: S53751  
 R:Pokkuluri, P.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.  
 J. Mol. Biol. 243, 283-297, 1994

A:Title: Preparation, characterization and crystallization of an antibody Fab fragment

A:Reference number: S53750; MUID:95018269; PMID:7523684

A:Accession: S53751

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-116 <POK>

A:Cross-references: UNIPROT:Q924P9; UNIPARC:UPI0000176DC3

C:Superfamily: immunoglobulin homology

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 21.3%; Score 129; DB 2; Length 116;  
Best Local Similarity 34.0%; Pred. No. 1.2e-05;  
Matches 33; Conservative 13; Mismatches 39; Indels 12; Gaps 2;

QY 19 SLRLDCRHEHTSSSNVMMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78

Db 17 SVKLSCKASGYFTFTSYMMQVQRPGGLEWIGEDPSDSTYNQKFKGKATLTVDTS 76

QY 79 SGHSPPISQNVTVLRDLKLVKCEGVY---RYFDY 111

Db 77 STAYMQLSSLT-----SEDSAVYYCANLGRYFDY 105

#### RESULT 9

S25175

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

A:Accession: S25175

R:Monestier, M.; Fasy, T.M.; Losman, M.J.; Novick, K.E.; Muller, S.

submitted to the EMBL Data Library, July 1992

A:Description: Structure and binding properties of monoclonal antibodies to core histone

A:Reference number: S25174

A:Accession: S25175

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <MON>

A:Cross-references: UNIPARC:UPI00001160C2; EMBL:X67620; NID:g51856; PIDN:CAA47878.1; PID

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 20.9%; Score 126.5; DB 2; Length 120;  
Best Local Similarity 33.3%; Pred. No. 2.1e-05;  
Matches 32; Conservative 18; Mismatches 41; Indels 5; Gaps 3;

QY 19 SLRLDCRHEHTSSSNVMMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78

Db 17 SVKLSCKASGYFTFTSYMMQVQRPGGLEWIGEDPSDSETHYNQKFKGKATLT--VDK 74

QY 79 SGHSPPISQNVTVLRDLKLVKCEGVYRY-YFDY 111

Db 75 SSNTAYMQLSSLTSEDSAVFYCAREKITDDYNYFDY 110

#### RESULT 10

S41394

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Jun-2000

A:Accession: S41394

R:Margaritte, C.; Gilbert, D.; Brard, F.; Tron, F.

submitted to the EMBL Data Library, January 1994

A:Description: Structural characterization of an (NZB X NZW) F1 mouse-derived IgM anti-DN

A:Reference number: S41393

A:Accession: S41394

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-120 <MAR>

A:Cross-references: UNIPARC:UPI00001165E2; EMBL:Z29586; NID:g452354; PIDN:CAA82703.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 20.8%; Score 126; DB 2; Length 120;  
Best Local Similarity 32.6%; Pred. No. 2.4e-05;  
Matches 31; Conservative 16; Mismatches 44; Indels 4; Gaps 2;

QY 19 SLRLDCRHEHTSSSNVMMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78

Db 17 SVKLSCKASGYFTFTSYMMQVQRPGGLEWIGEDPSDSTYNQKFKGKATLT--VDK 74

QY 79 SGHSPPISQNVTVLRDLKLVKCEGVY--RYFDY 111

Db 75 SSNTAYMQLSSLTSEDSAVFYCARRYGSRVSMY 109

#### RESULT 11

S25150

Ig heavy chain V region (AC38 260.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 16-Aug-1996

A:Accession: D25150

R:Didrop, R.; Bovens, J.; Siekevitz, M.; Beyreuther, K.; Rajewsky, K.

EMBO J. 3, 517-523, 1984

A:Title: A V region determinant (idiotope) expressed at high frequency in B lymphocytes

A:Reference number: A91000; MUID:84182519; PMID:6201362

A:Accession: D25150

A:Molecule type: protein

A:Residues: 1-89 <DIL>

A:Cross-references: UNIPARC:UPI00001769E1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 20.5%; Score 124; DB 2; Length 69;  
Best Local Similarity 41.8%; Pred. No. 2e-05;  
Matches 23; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 19 SLRLDCRHEHTSSSNVMMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYT 73

Db 5 SVKLSCKASGYFTFTSYMMQVQRPGGLEWIGEDPSDSTYNQKFKGKATLT 59

#### RESULT 12

S25036

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-Feb-1994 #sequence\_revision 01-Dec-1995 #text\_change 20-Jun-2000

A:Accession: S25036

R:Jacob, J.; Kelsos, G.

submitted to the EMBL Data Library, July 1992

A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny

A:Reference number: S25024

A:Accession: S25036

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-106 <JAC>

A:Cross-references: UNIPARC:UPI00001160B0; EMBL:X67373; NID:g50085; PIDN:CAA47785.1; PI

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:6-89/Domain: immunoglobulin homology <IMM>

Query Match 20.3%; Score 123; DB 2; Length 106;  
Best Local Similarity 32.3%; Pred. No. 4e-05;  
Matches 30; Conservative 13; Mismatches 48; Indels 2; Gaps 1;

QY 19 SLRLDCRHEHTSSSNVMMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTCALHH 78

Db 8 SVKLSCKASGYFTFTSYMMQVQRPGGLEWIGRIDPSNGGTYKYNKFKGKATLTVDKPS 67

QY 79 SGHSPPISQNVTVLRDLKLVKCEGVYRYFDY 111

Db 68 STAYMQLSS--LTSEDSAVFYCARYYGSYFDY 98

#### RESULT 13

S20646  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
 C:Accession: S20646  
 R:Loaman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.  
 submitted to the EMBL Data Library, February 1992  
 A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react  
 A:Reference number: S20639  
 A:Accession: S20646  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-123 <LOS>  
 A:Cross-references: UNIPARC:UPI0000116020; EMBL:X65001; NID:g52612; PIDN:CAA46134.1; PID  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 122.5; DB 2; Length 123;  
 Best Local Similarity 30.9%; Pred. No. 5.3e-05;  
 Matches 30; Conservative 16; Mismatches 36; Indels 15; Gaps 3;

QY 19 SLRLDCRHEHTSSSNYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTTCALHH 78

DB 17 SVKLSCKASGYFTTNIHVKRPGQGLEWIGETIAPSNDYTYNQNFKDKATLTVD--- 73

QY 79 SGHSPPISSQNVTLRLDKVKCE--GVYY---RYVFD 110

DB 74 -----KSNYAYQLSLSLTSDSAIYICSRRYVD 103

# RESULT 14

PH1164  
 Ig heavy chain V region (clone 37F.2A) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PH1164  
 R:Schitteck, B.; Rajewsky, K.  
 J. Exp. Med. 176, 427-438, 1992  
 A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.  
 A:Reference number: PH1105; MUID:92364545; PMID:1500855  
 A:Accession: PH1164  
 A:Molecule type: DNA  
 A:Residues: 1-98 <SCH>  
 A:Cross-references: UNIPARC:UPI0000176BC6  
 A:Experimental source: B cell  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 122; DB 2; Length 98;  
 Best Local Similarity 41.8%; Pred. No. 4.6e-05;  
 Matches 23; Conservative 10; Mismatches 22; Indels 0; Gaps 0;

QY 19 SLRLDCRHEHTSSSNYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYT 73

DB 17 SVKLSCKASGYFTTNIHVKRPGQGLEWIGETIAPSNDYTYNQNFKDKATLTV 71

# RESULT 15

S25054  
 Ig heavy chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 25-Feb-1994 #sequence\_revision 01-Dec-1995 #text\_change 20-Jun-2000  
 C:Accession: S25054  
 R:Jacob, J.; Kelsoe, G.  
 submitted to the EMBL Data Library, July 1992  
 A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny  
 A:Reference number: S25024  
 A:Accession: S25054  
 A:Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-111 <JAC>

A:Cross-references: UNIPARC:UPI00001160A4; EMBL:X67358; NID:g50921; PIDN:CAA47771.1; PID  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 20.2%; Score 122; DB 2; Length 111;  
 Best Local Similarity 32.3%; Pred. No. 5.3e-05;  
 Matches 30; Conservative 13; Mismatches 48; Indels 2; Gaps 1;

QY 19 SLRLDCRHEHTSSSNYMHFSLTRTKKHVLFGTIDPADSYTSYNQNFKDEGTYTTCALHH 78

DB 13 SVKLSCKASGYFTTNIHVKRPGQGLEWIGRIDPNSGGTKYNEKFSKATLTVDKPS 72

QY 79 SGHSPPISSQNVTLRLDKVKCEGVYYRYVFDY 111

DB 73 STAYMQLSS--LTSEDSAVYYCARYYGYGYFDY 103

Search completed: December 6, 2005, 10:42:44  
 Job time : 19.5645 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2005, 10:32:17 ; Search time 87.0209 Seconds  
(without alignments)  
532.965 Million cell updates/sec

Title: US-10-611-655-4  
Perfect score: 605  
Sequence: 1 QVSRGQKVTSLTACLVDSQL.....VLRDKLVKCEGVYRYFYDY 111

Scoring table: BLQSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	605	100.0	111	5	US-10-611-655-4
2	425	70.2	159	4	US-10-322-281-20
3	424	70.1	161	4	US-10-165-603-32
4	424	70.1	161	4	US-10-794-899-66
5	424	70.1	161	5	US-10-287-436A-449
6	424	70.1	161	5	US-10-287-436A-1149
7	424	70.1	165	3	US-09-925-301-1384
8	424	70.1	165	4	US-10-106-698-4624
9	422	69.8	161	3	US-09-918-715-220
10	422	69.8	161	4	US-10-474-794-220
11	422	69.8	161	5	US-10-979-159-220
12	402.5	66.5	162	5	US-10-611-655-1
13	398	65.8	176	5	US-10-611-655-10
14	398	65.8	334	5	US-10-611-655-6
15	398	65.8	334	5	US-10-611-655-8
16	293.5	48.5	158	4	US-10-322-281-17
17	291.5	48.2	162	3	US-09-918-715-303
18	291.5	48.2	162	4	US-10-474-794-303
19	291.5	48.2	162	5	US-10-979-159-303
20	291	48.1	171	5	US-10-450-763-49897
21	280	46.3	161	4	US-10-165-603-30
22	280	46.3	161	4	US-10-794-899-64
23	264.5	43.7	114	4	US-10-410-842A-4
24	186.5	30.8	124	5	US-10-611-655-2
25	162	26.8	51	5	US-10-450-763-49895
26	129.5	21.4	118	5	US-10-816-938-23
27	127.5	21.1	117	5	US-10-683-547-14

28	126	20.8	120	4	US-10-096-246-12	Sequence 12, Appl
29	124.5	20.6	116	3	US-03-940-727B-17	Sequence 17, Appl
30	123	20.3	113	3	US-09-940-727B-118	Sequence 118, Appl
31	123	20.3	121	5	US-10-879-994-82	Sequence 82, Appl
32	123	20.3	242	4	US-10-259-087A-18	Sequence 18, Appl
33	123	20.3	242	4	US-10-689-006-18	Sequence 18, Appl
34	123	20.3	248	5	US-10-879-994-14	Sequence 14, Appl
35	123	20.3	248	5	US-10-610-452-14	Sequence 14, Appl
36	119.5	19.8	464	4	US-10-216-484-9	Sequence 9, Appl
37	119.5	19.8	464	4	US-10-384-933-9	Sequence 9, Appl
38	118	19.5	104	6	US-11-032-482-1	Sequence 1, Appl
39	118	19.5	104	6	US-11-129-359-1	Sequence 1, Appl
40	118	19.5	121	4	US-10-643-857-2	Sequence 2, Appl
41	118	19.5	121	5	US-10-524-134-2	Sequence 2, Appl
42	116	19.2	114	4	US-10-803-622-226	Sequence 226, Appl
43	116	19.2	114	4	US-10-803-653-226	Sequence 226, Appl
44	116	19.2	118	5	US-10-937-046-9	Sequence 9, Appl
45	115.5	19.1	145	4	US-10-216-484-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1  
US-10-611-655-4  
; Sequence 4, Application US/10611655  
; Publication No. US2004026693A1  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Glen A.  
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides  
; FILE REFERENCE: 66863-026  
; CURRENT APPLICATION NUMBER: US/10/611,655  
; CURRENT FILING DATE: 2003-06-30  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: ThyOx non-immunoglobulin binding polypeptide  
US-10-611-655-4

Query Match	100.0%	Score 605;	DB 5;	Length 111;
Best Local Similarity	100.0%	Pred. No. 1e-56;		
Matches 111;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	QVSRGQKVTSLTACLVDSQLRDLCHRENTSSNYMWFSLTRETXXHVLFGTIDPADSYT	60	
Db	1	QVSRGQKVTSLTACLVDSQLRDLCHRENTSSNYMWFSLTRETXXHVLFGTIDPADSYT	60	
QY	61	SYNQNFQDEGTYTCALHSHGSPPISSQNVTVLRDKLVKCEGVYRYFYDY	111	
Db	61	SYNQNFQDEGTYTCALHSHGSPPISSQNVTVLRDKLVKCEGVYRYFYDY	111	
RESULT 2				
US-10-322-281-20				
; Sequence 20, Application US/10322281				
; Publication No. US20040126762A1				
; GENERAL INFORMATION:				
; APPLICANT: David W. Morris				
; APPLICANT: Marc S. Malandaro				
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer				
; FILE REFERENCE: 529452001000				
; CURRENT APPLICATION NUMBER: US/10/322,281				
; CURRENT FILING DATE: 2002-12-17				
; NUMBER OF SEQ ID NOS: 866				
; SOFTWARE: FastSeq for Windows Version 4.0				
; SEQ ID NO 20				
; LENGTH: 159				
; TYPE: PRT				
; ORGANISM: Homo sapiens				





Db 15 QVSRGQKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRTKKHVLFGTGVPPEHTY 74  
QY 60 TSYNQNF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGV 103  
Db 75 RS-RTNFTSKYHKMVLVLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGI 133

RESULT 11  
US-10-979-159-220  
; Sequence 220, Application US/10979159  
; Publication No. US20050142138A1  
; GENERAL INFORMATION:  
; APPLICANT: Brad St. Croix  
; APPLICANT: Bert Vogelstein  
; APPLICANT: Kenneth Kinzler  
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS  
; FILE REFERENCE: 1107.00134  
; CURRENT APPLICATION NUMBER: US/10/979,159  
; CURRENT FILING DATE: 2004-11-03  
; PRIOR APPLICATION NUMBER: US/09/918,715  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/222,599  
; PRIOR FILING DATE: 2000-08-02  
; PRIOR APPLICATION NUMBER: 60/224,360  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: 60/282,850  
; PRIOR FILING DATE: 2000-04-11  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 220  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-979-159-220

Query Match 69.8%; Score 422; DB 5; Length 161;  
Best Local Similarity 73.3%; Pred. No. 6e-37;  
Matches 88; Conservative 3; Mismatches 11; Indels 18; Gaps 3;  
QY 1 QVSRGQKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRTKKHVLFGTID-PADSY 59  
Db 15 QVSRGQKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRTKKHVLFGTGVPPEHTY 74  
QY 60 TSYNQNF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGV 103  
Db 75 RS-RTNFTSKYHKMVLVLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGI 133

RESULT 12  
US-10-611-655-1  
; Sequence 1, Application US/10611655  
; Publication No. US20040266993A1  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Glen A.  
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides  
; FILE REFERENCE: 66663-026  
; CURRENT APPLICATION NUMBER: US/10/611,655  
; CURRENT FILING DATE: 2003-06-30  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 162  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-611-655-1

Query Match 66.5%; Score 402.5; DB 5; Length 162;  
Best Local Similarity 71.9%; Pred. No. 7.4e-35;  
Matches 87; Conservative 3; Mismatches 12; Indels 19; Gaps 4;  
QY 1 QVSRGQKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRTKKHVLFGTID-PADSY 59

Db 15 QVSRGQKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRTKKHVLFGTGVPPEHTY 74  
QY 60 TSYNQNF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGI 102  
Db 75 RS-RTNFTSKYHKMVLVLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGI 133  
QY 103 V 103  
Db 134 I 134

RESULT 13  
US-10-611-655-10  
; Sequence 10, Application US/10611655  
; Publication No. US20040266993A1  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Glen A.  
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides  
; FILE REFERENCE: 66663-026  
; CURRENT APPLICATION NUMBER: US/10/611,655  
; CURRENT FILING DATE: 2003-06-30  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chimeric ThyOx carrier polypeptide containing  
; OTHER INFORMATION: glucagon-like peptide 1  
US-10-611-655-10

Query Match 65.8%; Score 398; DB 5; Length 176;  
Best Local Similarity 72.2%; Pred. No. 2.5e-34;  
Matches 83; Conservative 3; Mismatches 11; Indels 18; Gaps 3;  
QY 6 QKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRTKKHVLFGTID-PADSYTSYQ 64  
Db 49 QKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRTKKHVLFGTGVPPEHTYRS-RT 107  
QY 65 NF-----KDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGV 103  
Db 108 NFTSKYHKMVLVLSAFTSKDEGTYTCALHSHGSHSPPISSQNVTVLRDKLVKCGI 162

RESULT 14  
US-10-611-655-6  
; Sequence 6, Application US/10611655  
; Publication No. US20040266993A1  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Glen A.  
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides  
; FILE REFERENCE: 66663-026  
; CURRENT APPLICATION NUMBER: US/10/611,655  
; CURRENT FILING DATE: 2003-06-30  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chimeric ThyOx carrier polypeptide containing  
; OTHER INFORMATION: erythropoietin  
US-10-611-655-6

Query Match 65.8%; Score 398; DB 5; Length 334;  
Best Local Similarity 72.2%; Pred. No. 5.3e-34;  
Matches 83; Conservative 3; Mismatches 11; Indels 18; Gaps 3;  
QY 6 QKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRTKKHVLFGTID-PADSYTSYQ 64  
Db 207 QKVTSLTACLVDSRLDCRHSNTSSPIQVEFSLTRTKKHVLFGTGVPPEHTYRS-RT 265

Qy 65 NP-----KDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGV 103  
||  
Db 266 NFKSKYHMKVLYLSAFTSKDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGI 320

RESULT 15

US-10-611-655-8  
; Sequence 8, Application US/10611655  
; Publication No. US20040266993A1  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Glen A.  
; TITLE OF INVENTION: Non-Immunoglobulin Binding Polypeptides  
; FILE REFERENCE: 66663-026  
; CURRENT APPLICATION NUMBER: US/10/611,655  
; CURRENT FILING DATE: 2003-06-30  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SuperEpo  
US-10-611-655-8

Query Match 65.8%; Score 398; DB 5; Length 334;  
Best Local Similarity 72.2%; Pred. No. 5.3e-34;  
Matches 83; Conservative 3; Mismatches 11; Indels 18; Gaps 3;

Qy 6 QKVTSLTACLVDQSLDCRHEHTSSNTYWMHPSLRTETKKHVLFGTID-PADSYTSYNO 64  
||  
Db 207 QKVTSLTACLVDQSLDCRHEHTSSNTYWMHPSLRTETKKHVLFGTGVPEHTYRS-RT 265

Qy 65 NP-----KDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGV 103  
||  
Db 266 NFKSKYHMKVLYLSAFTSKDEGTYTCALHSHGSPPISSQNVTVLRDLKLVKCEGI 320

Search completed: December 6, 2005, 10:47:47  
Job time : 88.0209 secs

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